

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 30, 2004, 14:49:24 ; Search time 5672.5 Seconds

(without alignments)
10716.922 Million cell updates/sec

Title: US-09-737-297-1

Sequence: 1 gttacgtcagattgacgct.....ctggggttgaagctacg 1486

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

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2: gb_hcg:
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4: gb_om:
5: gb_ov:
6: gb_pac:
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11: gb_sts:
12: gb_sy:
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14: gb_vl:
15: em_ba:
16: em_fun:
17: em_hum:
18: em_in:
19: em_mu:
20: em_om:
21: em_or:
22: em_ov:
23: em_ph:
24: em_pac:
25: em_pl:
26: em_ro:
27: em_sts:
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32: em_hcg_other:
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36: em_hcg_mam:
37: em_hcg_vrt:
38: em_sy:
39: em_higo_hum:
40: em_higo_mus:
41: em_higo_other:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1486	100.0	1486	1	MPR238597
2	1486	100.0	1486	6	AX175613
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9	1272	85.6	1455	1	AY028204
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ALIGNMENTS

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ACCESSION	AJ238597				
VERSION	AJ238597.1	GI:4741661			
KEYWORDS	16S ribosomal RNA; 16S rRNA gene.				
SOURCE	Marinomonas protea				
ORGANISM	Marinomonas protea				
REFERENCE	Marinomonas protea				
AUTHORS	Mills, S.V., Stewart, G.S.A.B., Laybourn-Parry, J. and Hill, P.C.				
TITLE	Marinomonas protea sp. nov., a novel Antarctic bacterium isolated from Ace Lake, Eastern Antarctica				

JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1486)
 AUTHORS Mills S.V.
 TITLE Direct Submission
 JOURNAL Submitted (28-APR-1999) Mills S.V., Food Microbiology, University
 of Nottingham, Sutton Bonington Campus, Leicestershire, LE12 5RD,
 UNITED KINGDOM

FEATURES
 source Location/Qualifiers

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 Matches 1486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DEFINITION Sequence 1 from Patent WO0144275.
 ACCESSION AX175613
 VERSION AX175613.1 GI:14598933
 KEYWORDS
 SOURCE
 ORGANISM
 Marinomonas protea
 Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales;
 Marinomonas.
 REFERENCE
 1 Berry M.J., Griffiths A.U., Hill P.J., Laybourne-Parry J. and
 Mills S.V.
 TITLE Processes and organisms for the production of anti-freeze proteins
 JOURNAL Patent: WO 0144275-A 1 21-JUN-2001;
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Matches 1486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ORGANISM uncultured bacterium
REFERENCE 1 (bases 1 to 1421)
AUTHORS Brinkmeyer, R. and Helmke, E.
TITLE Evidence for methyloleotrophic processes in Arctic pack ice
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 1421)
Brinkmeyer, R. and Helmke, E.
TITLE Direct Submission
JOURNAL Submitted (14-JAN-2002) Pelagic Oceanography,
Alfred-Wegener-Institut fuer Polar und Meeresforschung, Am
Handelsnafen 12, Bremerhaven D-27570, Germany
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RESULT 4
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sequence.
ACCESSION AF468385
VERSION AF468385.1 GI:28269033
KEYWORDS
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Arctic sea ice bacterium ARK10032
Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales;
Madinomonas.
REFERENCE 1 (bases 1 to 1425)
AUTHORS Brinkmeyer, R. and Helmke, E.
TITLE Diversity of bacteria in Arctic sea ice
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1425)
AUTHORS Brinkmeyer, R. and Helmke, E.
TITLE Direct Submission
JOURNAL Submitted (15-JAN-2002) Pelagic Oceanography,
Alfred-Wegener-Institut fuer Polar und Meeresforschung, Am
Handels Hafen 12, Bremerhaven D-27570, Germany
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DB 62 GAATCTGCTGTGTAAGAGGAGGAGCAACATGTGAAAGCATGTCTAATACCGCATACCGCT 121

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QY 168 GAGGGGAGAAAGAGGGGACTCTTGAGAGCCCTCCGCTATTAGATGAGCTGCGTGAAT 227
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QY 228 AGTAGATTGGATGGGTAAAGGCTTACCAAGCGACAGATCTTAACCTGATCTGAGAGATG 287
DB 182 AGTAGATTGGATGGGTAAAGGCTTACCAAGCGACAGATCTTAACCTGATCTGAGAGATG 241
QY 288 ACCAGTCACTGGGATCTGAGACACGCGCCAGCTCTTACGGGAGGACAGCTGGGGAAT 347
DB 242 ACCAGTCACTGGGATCTGAGACACGCGCCAGCTCTTACGGGAGGACAGCTGGGGAAT 301
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QY 408 TTGTAAAGCACTTTCAGGGGTGAGGAAAGGTGATAGGTTAATCGTTATCATCTTGACGT 467
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QY 768 GATTAGATACCCCTGTGTAGTCCAGCGGTAAAGATGCTAATACCGCTTGGTGTATATG 827
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QY 828 ACTTAGTGGCGAGCTTAACGCAATAGTAGACCGCTGAGGATACGCGCGCAAGTTAA 887
DB 782 ACTTAGTGGCGAGCTTAACGCAATAGTAGACCGCTGAGGATACGCGCGCAAGTTAA 841
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DB 902 AACCGAAGAACTTACCTTACTCTTGACATCCACAGAACTTTGAGATGATGATGTGC 961
QY 1008 CTTTGGGAACTGTGAGACAGGTGCTGATGTGTGTGTGTAAGTGTGTTG 1067
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LOCUS
DEFINITION
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sequence.
ACCESSION
AY092066.1 GI:20152166
VERSION
AY092066.1
KEYWORDS
Marinomonas protea
SOURCE
Marinomonas protea
ORGANISM
Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales;
Marinomonas

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REFERENCE
1 (bases 1 to 1372)
AUTHORS
Gilbert,J.A., Laybourn-Parry,J., Hill,P.J. and Dodd,C.
TITLE
Novel bacterial strains from Antarctic lakes
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 1372)
AUTHORS
Gilbert,J.A., Laybourn-Parry,J., Hill,P.J. and Dodd,C.
TITLE
Direct Submission
JOURNAL
Submitted (27-MAR-2002) Life and Environmental Science, University
of Nottingham, Sutton Bonington Campus, Sutton Bonington, Leics
LE12 5RD, England

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 Db 1012 GGTGAGGAAGGGGTAGTAAATCATTATCTTTCAGTTCAGTCCCGAAGAAAGAC 953
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 DEFINITION
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 sequence, strain: KMM 3634.
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 AB074194
 VERSION
 AB074194.1 GI:18143647
 KEYWORDS
 Marimonas primoryensis
 Marimonas primoryensis
 Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales;
 Marimonas.
 REFERENCE
 1
 Romanenko, L.A., Uchino, M., Mikhailov, V.V., Zhukova, N.V. and
 Uchimura, T.
 Marimonas primoryensis sp. nov., a novel psychrophile isolated
 from coastal sea ice in the Sea of Japan
 Int. J. Syst. Evol. Microbiol. 53, 829-832 (2003)
 2 (bases 1 to 1449)
 Uchino, M., Uchimura, T. and Romanenko, L.A.
 Direct Submission
 Submitted (12-NOV-2001) Masataka Uchino, Tokyo University of
 Agriculture, Department of Applied Biology and Chemistry,
 Sakuragaoka 1-1-1, Setagaya-ku, Tokyo 158-8502, Japan
 (E-mail: muchino@nodai.ac.jp, Tel: 81-3-5477-2324,
 Fax: 81-3-5477-2619)
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LOCUS AB074193
DEFINITION Marinomonas primoryensis gene for 16S ribosomal RNA, partial
ACCESSION AB074193
VERSION AB074193.1 GI:18143646
KEYWORDS

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REFERENCE
AUTHORS
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 DEFINITION Marinomonas communis 16S ribosomal RNA ribosomal RNA gene, partial
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 ACCESSION AF173967 GI:9622547
 VERSION AF173967.1
 KEYWORDS
 SOURCE
 ORGANISM
 Marinomonas communis
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 Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales;
 Marinomonas
 1 (bases 1 to 1448)
 Elmers, R.; Bernthaler, J.; Glockner, F. O. and Amann, R.
 Reference
 Authors
 Title
 Cultureability and in situ abundance of pelagic bacteria from the

North Sea
 Appl. Environ. Microbiol. 66 (7), 3044-3051 (2000)
 MEDLINE
 20336458
 PUBMED
 10877804
 REFERENCE
 2 (bases 1 to 1448)
 AUTHORS
 Elmers, R.
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LOCUS
DEFINITION Marine Bacterium Tw-9 16S ribosomal RNA gene, partial sequence.
ACCESSION AY028204
VERSION AY028204.1 GI:13660692
KEYWORDS

SOURCE
ORGANISM
marine bacterium Tw-9
marine bacterium Tw-9
Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales;
Halomonadaceae.

REFERENCE
AUTHORS Bidle, K.D. and Azam, F.
TITLE Bacterial control of silicon regeneration from diatom detritus:
JOURNAL Limnol. Oceanogr. 46 (7), 1606-1623 (2001)
REFERENCE 2 (bases 1 to 1455)

AUTHORS Bidle, K.D. and Azam, F.
TITLE Direct Submission
JOURNAL Submitted (01-MAR-2001) Scripps Institution of Oceanography,
University of California San Diego, 9500 Gilman Drive, La Jolla, CA
92093-0202, USA

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Qy 854 GTAGACCGCTGAGGAGTACGGCGCAGAGTTAAATCAATGATGACGGGGGCGG 913
Db 840 GTAGACCGCTGAGGAGTACGGCGCAGAGTTAAATCAATGATGACGGGGGCGG 899

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LOCUS Marimonas mediterranea strain MMB-1.16S ribosomal RNA gene,
DEFINITION complete sequence.
ACCESSION AF063027
VERSION AF063027.1 GI:3929025
KEYWORDS Marimonas mediterranea
SOURCE Marimonas mediterranea
ORGANISM Marimonas mediterranea; Gammaproteobacteria; Oceanospirillales;
Marimonas.
REFERENCE 1 (bases 1 to 1534)
AUTHORS Solano, F. and Sanchez-Amat, A.
TITLES Studies on the phylogenetic relationships of melanogenic marine
bacteria: proposal of Marimonas mediterranea sp. nov
JOURNAL Int. J. Syst. Bacteriol. 49 Pt 3, 1241-1246 (1999)
MEDLINE 9934518
PubMed 10425786
REFERENCE 2 (bases 1 to 1534)
AUTHORS Sanchez-Amat, A. and Solano, F.
TITLES Direct Submission
JOURNAL Submitted (04-MAY-1998) Genetics and Microbiology, Faculty of
Biology, University of Murcia, Campus de Espinardo, Murcia 30100,
Spain
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VERSION	AY028196.1	GI:13660684		
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ORGANISM	Bacteria; Proteobacteriia; Gammaproteobacteriia; Oceanospirillales; Halomonadaceae;			
REFERENCE	1. (bases 1 to 1475)			
AUTHORS	Bidle,K.D. and Azam,F.			
TITLE	Bacterial control of siliicon regeneration from diatom detritus:			
JOURNAL	Significance of bacterial ecdhydrolases and species identity			
REFFERENCE	Limnol. Oceanogr. 46 (7), 1606-1623 (2001)			
AUTHORS	2. (bases 1 to 1475)			
TITLE	Bidle,K.D. and Azam,F.			
JOURNAL	Direct Submision			
REFFERENCE	Submitted (01-MAR-2001) Scripps Institution of Oceanography,			
	University of California San Diego, 9500 Gilman Drive, La Jolla, CA			
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Qy	316	CCAGATCTCTACGGGAGGACAGTGGGGAAATTGACAAATGGGCGCAAGCTTATCCA	375	
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LOCUS AX175616
DEFINITION Sequence 4 from Patent WO0144275.
ACCESSION AX175616
VERSION AX175616.1 GI:14598935
KEYWORDS
SOURCE
ORGANISM
Marinomonas communis
Marinomonas communis
Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales;
Marinomonas.

REFERENCE
AUTHORS
1 Berry, M.J., Griffiths, A.U., Hill, P.J., Laybourne-Parry, J. and
Hillis, S.V.
TITLE
JOURNAL
Processes and organisms for the production of anti-freeze proteins
Patent: WO 0144275-A 4 21-JUN-2001;
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Query Match 84.2%; Score 1251.8; DB 6; Length 1481;
Best Local Similarity 93.7%; Pred. No. 0;
Matches 1374; Conservative 1; Mismatches 83; Indels 9; Gaps 7;

Qy 3 TAGCTCAGATTGAACTGCGCGAGGCTTAAACATGCAAGTCAAGCGGTAAACAGGG 62
Db 21 TGGCTCAGATTGAACTGCGCGAGGCTTAAACATGCAAGTCAAGCGGTAAACATTC 79
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Db 80 TAGCTTCTAGAAAGATGAGAGCGCGGAGCGGTGATGAGCGGTGAGAAATCTGCTAGT 139
Qy 121 AGAGGGGGAACAATGTGAAAAGCAATGCTAATACCGCATACGCGCTTACGAGGGAAGA 180
Db 140 AGAGGGGGAACAATGTGAAAAGCAATGCTAATACCGCATACGCGCTTACGAGGGAAGA 199
Qy 181 GGGAGACTTTCGAGCCTTCGGCTATTAGATGAGCTGCGTGAAGATTAGCTAGTGGTAG 240

Db 200 GGG--NNTCTTCGACACTTTCGCTATTATTAATGAGCTGCTGATGATTAAGTGTGG 257
Qy 241 GGTAAAGGCTTACCAAGGCGACATCTTAAGTGTCTGAGAGATGACCACTG 300
Db 258 GGTAAAGGCTTACCAAGGCGACATCTTAAGTGTCTGAGAGATGATCAACACACTG 317
Qy 301 GGAAGTGAACGGGCCCAAGCTCTACGGGAGGCGACAGTGGGGAATATTGACATGG 360
Db 318 GGAAGTGAACGGGCCCAAGCTCTACGGGAGGCGACAGTGGGGAATATTGACATGG 377
Qy 361 CGAAGCTGATCAAGCAATGCGCGTGTGTAAGAGGCTTAAAGGCTTAAAGCACTT 420
Db 378 CGAAGCTGATCAAGCAATGCGCGTGTGTAAGAGGCTTAAAGGCTTAAAGCACTT 437
Qy 421 TCAAGGTTGAGAGGTTGATGATGATTAATACCTTCACTGAGGTTAGCCGAGAGA 480
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Qy 481 AGCACCGGCTAACCTGTGTGCAAGCGCGGTAAATACAGAGGTTGCAAGCGTTAATCG 540
Db 498 AGCACCGGCTAACCTGTGTGCAAGCGCGGTAAATACAGAGGTTGCAAGCGTTAATCG 557
Qy 541 AATTACTGGGCTTAAGCGCGGTAGTGTGTTAAGTCCGATGTAATCCCAAGGCG 600
Db 558 AATTACTGGGCTTAAGCGCGGTAGTGTGTTAAGTCCGATGTAATCCCAAGGCG 617
Qy 601 TCAACTTGAATGCAACCGGCTACTGCTAGCTAGATGATGATGAGGAGGTTGGAATT 660
Db 618 TCAACTTGAATGCAACCGGCTACTGCTAGCTAGATGATGATGAGGAGGTTGGAATT 677
Qy 661 TCTGTGTAGGCGTGAATATGCTGATATAGAGGAACATCAAGTGGCGAAGCGCACAC 720
Db 678 TCTGTGTAGGCGTGAATATGCTGATATAGAGGAACATCAAGTGGCGAAGCGCACAC 737
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Db 738 CTGAGCTAATACCTGACACTGAGGTCGAAAGCGTGGGAGCAACAGATTAATACCT 797
Qy 781 GGTAGTCCAGCGCTTAACGATGTCTAAGCCGTT -GGGTTGTAATGACTTAAGTGGCG 839
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Qy 900 TTGACGGGCGCCGACAGCGGTGAGCATGTGTTAATTGAAACAAACGGAAGAAC 959
Db 918 TTGACGGGCGCCGACAGCGGTGAGCATGTGTTAATTGAAANNAACGGAAGAAC 977
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AF321017 1343 bp DNA linear BCT 05-MAY-2003

LOCUS AF321017

DEFINITION Marinomonas sp. GOBB3-320 16S ribosomal RNA gene, partial sequence.

ACCESSION AF321017

VERSION AF321017.2 GI:30158656

KEYWORDS

SOURCE Marinomonas sp. GOBB3-320

ORGANISM Marinomonas sp. GOBB3-320

Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales; Marinomonas.

REFERENCE 1 (bases 1 to 1343)

AUTHORS Kisanand, V., Cuadros, R. and Wikner, J.

TITLE Phylogeny of culturable estuarine bacteria catbolizing riverine organic matter in the northern Baltic Sea

JOURNAL Appl. Environ. Microbiol. 68 (1), 379-388 (2002)

MEDLINE 21633837

PUBMED 11772648

REFERENCE 2 (bases 1 to 1343)

AUTHORS Kisanand, V., Cuadros, R. and Wikner, J.

TITLE Direct Submission

JOURNAL Submitted (11-NOV-2000) Department of Microbiology, University of Umea, Umea S-90187, Sweden

REFERENCE 3 (bases 1 to 1343)

AUTHORS Kisanand, V., Cuadros, R. and Wikner, J.

TITLE Direct Submission

JOURNAL Submitted (28-APR-2003) Department of Microbiology, University of Umea, Umea S-90187, Sweden

REMARK Nucleotide sequence updated by submitter

COMMENT On Apr 28, 2003 this sequence version replaced gi:13336278.

FEATURES

source

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location/Qualifiers

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/db_xref="taxon:151201"

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/product="16S ribosomal RNA"

BASE COUNT 351 a 299 c 416 g 277 t

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Query Match 80.6%; Score 1197.8; DB 1; Length 1343;

Best Local Similarity 95.1%; Pred. No. 0;

Matches 1279; Conservative 0; Mismatches 62; Indels 4; Gaps 4;

QY 74 GCTGACGAGCGCGGAGCGGTGAGTAAAGCGGTAGATCTGCTAGTAGAGGGGAGCAAC 133

Db 1 GGTGACGAGCGCGGAGCGGTGAGTAAAGCGGTAGATCTGCTAGTAGAGGGGAGCAAC 60

QY 134 ATGTGAAACGCGATGCTAATACCGCATACGCCCTTGAGGGGAAAGAGGGGACTTTGGG 193

Db 61 ATGTGAAACGCGATGCTAATACCGCATACGCCCTTGAGGGGAAAGAGGGGACTTTGGG 120

QY 194 AGCTTCGCGTATTAAGTAGAGCTGCGTGAAGATTAGCTAGTGTGAGGTAAGGCTTAC 253

Db 121 AGCTTCGCGTATTAAGTAGAGCTGCGTGAAGATTAGCTAGTGTGAGGTAAGGCTTAC 180

QY 254 CAAGCGAGATCTTAAGTGTGAGAGAGTAGACAGTCACTCGGAGCTGAGACAG 313

Db 181 CAAGCGAGATCTTAAGTGTGAGAGAGTAGACAGTCACTCGGAGCTGAGACAG 240

QY 314 GCCAGACTCTTACCGGAGGAGCAGAGTGGGGAATATTGACATGGCGCAAGCTTATC 373

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Db 361 AAGGTGATAGGTTAATACGTTATCATCTTGACGTTAGCCCAAGAAAGACCGGCTTAC 420

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Db 421 TCTGTGCCAGAGCCCGCGGTAAATACAGAGGTTGAAGCGTTAATGGAATTTACTGGGCGT 480

QY 554 AAGCGCGGTAGTGTGTTGTTAAGTCGATGTGAATCCAGAGGCTCAACCTTGAAT 613

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QY 734 GACACTGAGTGCAGAAAGCGTGGGAGCAAAACAGATTAAATACCCTGTGTACAGCC 793

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Db 780 AAGTAGACCGCTGGGAGGATACGGCCGCAAGGTTAAATCTCAATTAATTAAGCGGGGCG 839

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RESULT 14
LOCUS MY16SRNA 1467 bp DNA linear BCT 06-JUN-2003
DEFINITION M.vaga 16S rRNA sequence.
ACCESSION X67025
VERSION X67025.1 GI:44693
KEYWORDS 16S-like rRNA.
SOURCE Marinomonas vaga
ORGANISM Marinomonas vaga
Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales; Marinomonas.
REFERENCE 1 (bases 1 to 1467)
AUTHORS Gauthier M.J., Lafay, B., Christen, R., Fernandez, L., Acquaviva, M., Bonin, P. and Bertrand, J.C.
TITLE Marinobacter hydrocarbonoclasticus gen. nov., sp. nov., a new, extremely halotolerant, hydrocarbon-degrading marine bacterium
JOURNAL Int. J. Syst. Bacteriol. 42 (4), 568-576 (1992)
MEDLINE 93002312
REFERENCE 2
AUTHORS Lafay, B.
TITLE Direct Submission
JOURNAL Submitted (17-JUN-1992) B. Lafay, URA 671 CNRS-Universite Paris VI, Station Zoologique, Villefranche-sur-Mer, 06230, FRANCE
COMMENT Alteromonas vaga is identical with Marinomonas vaga.
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BASE COUNT 379 a 318 c 454 g 312 t 4 others
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Query Match 80.1%; Score 1190.2; DB 1; Length 1467;
Best Local Similarity 92.5%; Pred. No. 0;
Matches 1349; Conservative 0; Mismatches 96; Indels 13; Gaps 9;

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Db 139 AATGGGGACACATGCTGAAACGATCTAAATACCGATACGCGCTGAGGGGAAAGGA 198
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RESULT 15
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LOCUS Uncultured bacterium clone ARKCH4-6 16S ribosomal RNA gene, partial
DEFINITION
ACCESSION AF468267
VERSION AF468267.1 GI:28268916
KEYWORDS
SOURCE uncultured bacterium
ORGANISM Bacteria; environmental samples.
REFERENCE 1 (bases 1 to 1417)
AUTHORS Brinkmeyer R. and Helmke, E.
TITLE Evidence for methylootrophic processes in Arctic pack ice
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1417)
AUTHORS Brinkmeyer R. and Helmke, E.
TITLE Direct Submission
JOURNAL Submitted (14-JAN-2002) Pelagic Oceanography,
Alfred-Wegener-Institut fuer Polar und Meeresforschung, Am
Handels Hafen 12, Bremerhaven D-27570, Germany
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Best Local Similarity 91.3%; Pred. No. 0;
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Db 1381 AGAAGTAGCTAGCTTAACTTGGG 1406

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Search completed: January 30, 2004, 22:02:53
Job time : 5677.5 secs

PT Preparing anti-freeze peptides useful in frozen food products, e.g.
 PT frozen vegetables and confectionery, by culturing bacteria from aqueous
 PT low-temperature environment and extracting anti-freeze proteins from
 PT culture -

XX Claim 2, Page 55, 59pp; English.

CC The present sequence represents the 16S rRNA of *Marinomonas protea*.
 CC Anti-freeze proteins can be isolated from *M. protea*, using the method
 CC of the invention. The specification describes a method for producing
 CC anti-freeze peptides (AFPs). The method comprises collecting one or
 CC more samples of bacteria from an aqueous low-temperature environment,
 CC culturing the bacteria and extracting proteins from the samples, testing
 CC the proteins for anti-freeze properties, selecting proteins having
 CC anti-freeze properties and producing the selected protein for use as
 CC an AFP food additive. The method is useful for producing AFPs which are
 CC incorporated in food products, such as frozen vegetables and frozen
 CC confectionery such as ice-cream. AFPs are useful in frozen food products,
 CC such as vegetables, sauces, soups, snacks, dairy products and frozen
 CC confectionery, which includes sorbet, water-ice, granites, frozen fruit
 CC purees and milk-containing frozen products such as ice-cream, frozen
 CC yogurt or custards, sherbet and ice-milk.

XX Sequence 1485 BP; 383 A; 325 C; 465 G; 312 T; 0 other;

Query Match 99.2%; Score 1474; DB 22; Length 1485;

Best Local Similarity 99.9%; Pred. No. 0; Mismatches 0; Indels 1; Gaps 1;

Matches 1485; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GTTAACTCAGATTGAACGCTGGCGGAGGCTTAAACATGACATGACGCGTAAACAG 60
 DB 1 GTTAACTCAGATTGAACGCTGGCGGAGGCTTAAACATGACATGACGCGTAAACAG 60
 QY 61 GGAAGTCT 120
 DB 61 GGAAGTCT 120
 QY 121 AGAGGGGAGCAACATGCTGGAACGATGCTATATCCGCATACGCGCTGAGGGGAAAGA 180
 DB 121 AGAGGGGAGCAACATGCTGGAACGATGCTATATCCGCATACGCGCTGAGGGGAAAGA 180
 QY 122 AGAGGGGAGCAACATGCTGGAACGATGCTATATCCGCATACGCGCTGAGGGGAAAGA 180
 DB 122 AGAGGGGAGCAACATGCTGGAACGATGCTATATCCGCATACGCGCTGAGGGGAAAGA 180
 QY 181 GGGGACTCTTGGGAGCTTCCGCTATATGATGAGCTTGGCTGATTAAGTAACTGCTG 240
 DB 181 GGGGACTCTTGGGAGCTTCCGCTATATGATGAGCTTGGCTGATTAAGTAACTGCTG 240
 QY 241 GGTAAAGGCTACCAAGGCGAGATCTCTATCTGATGAGAGATGACCATGACACATG 300
 DB 241 GGTAAAGGCTACCAAGGCGAGATCTCTATCTGATGAGAGATGACCATGACACATG 300
 QY 242 GGTAAAGGCTACCAAGGCGAGATCTCTATCTGATGAGAGATGACCATGACACATG 300
 DB 242 GGTAAAGGCTACCAAGGCGAGATCTCTATCTGATGAGAGATGACCATGACACATG 300
 QY 301 GGAAGTGAACACGAGCCGAGACTCTTACCGGAGGAGGAGAGATGAGCAATGCG 360
 DB 301 GGAAGTGAACACGAGCCGAGACTCTTACCGGAGGAGGAGAGATGAGCAATGCG 360
 QY 361 GCGAAGCTGATCCGAGCCATGCGCGTGTGAGAGAGGCTTAAAGGCTTAAAGCACTT 420
 DB 361 GCGAAGCTGATCCGAGCCATGCGCGTGTGAGAGAGGCTTAAAGGCTTAAAGCACTT 420
 QY 421 TCAGGGGTGAGGAGGATGATAGTTATACGTTATCATCTTGAAGTAAAGCAAG 480
 DB 421 TCAGGGGTGAGGAGGATGATAGTTATACGTTATCATCTTGAAGTAAAGCAAG 480
 QY 481 AGCAGCGGCTAATCTTGTGCGAGCAGCGCGGCTATATCAGAGGCTGAAAGCTTAACTG 540
 DB 481 AGCAGCGGCTAATCTTGTGCGAGCAGCGCGGCTATATCAGAGGCTGAAAGCTTAACTG 540
 QY 541 AATTAAGTGAAGGAGGCGGCTGATGATGATGATGATGATGATGATGATGATGATGAT 600
 DB 541 AATTAAGTGAAGGAGGCGGCTGATGATGATGATGATGATGATGATGATGATGATGAT 600
 QY 601 TCAACTTGAATGAGCAACCGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
 DB 601 TCAACTTGAATGAGCAACCGATGATGATGATGATGATGATGATGATGATGATGATGAT 660

QY 661 TCCTGTGTAGCCGTGTAATGCGTATATAGAGAGAAATCATGATGCGGAGCGACACC 720
 DB 661 TCCTGTGTAGCCGTGTAATGCGTATATAGAGAGAAATCATGATGCGGAGCGACACC 720
 QY 721 CTGAGCTAATATGACATGACATGAGGTGAGAAAGGCGGAGGAGCAACAGATTATGATCCCT 780
 DB 721 CTGAGCTAATATGACATGACATGAGGTGAGAAAGGCGGAGGAGCAACAGATTATGATCCCT 780
 QY 781 GGTATGTCAGCGCGGTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
 DB 781 GGTATGTCAGCGCGGTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
 QY 841 GCTAAGCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
 DB 841 GCTAAGCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
 QY 901 TGAAGGGGGGCGCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
 DB 901 TGAAGGGGGGCGCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
 QY 961 TTAAGCTTCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
 DB 961 TTAAGCTTCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
 QY 1021 GAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
 DB 1021 GAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
 QY 1081 AACGAGGCAACCTTGTCTTATTTTCCAGAGCATGATGATGATGATGATGATGATGATGAT 1140
 DB 1081 AACGAGGCAACCTTGTCTTATTTTCCAGAGCATGATGATGATGATGATGATGATGATGAT 1140
 QY 1141 GCGGGTACAAACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
 DB 1141 GCGGGTACAAACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
 QY 1201 GGGGCTACACGCTGCTACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
 DB 1201 GGGGCTACACGCTGCTACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
 QY 1261 ATCCGCAAAAGTACGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
 DB 1261 ATCCGCAAAAGTACGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
 QY 1321 ATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
 DB 1321 ATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
 QY 1381 GCGCCGTCACACATGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
 DB 1381 GCGCCGTCACACATGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
 QY 1441 GCGCGTTACACAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1486
 DB 1441 GCGCGTTACACAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1486

RESULT 2
 AA164997
 ID AA164997 standard; DNA; 1501 BP.
 XX AA164997;
 AC
 XX
 DT 11-DEC-2001 (first entry)
 XX
 XX Polyhydroxyalkanoic acid related *Pseudomonas jessenii* coding sequence.
 DE Polyhydroxyalkanoic acid; PHA; functional polymer; ds.
 XX
 XX Pseudomonas jessenii.
 OS
 XX
 XX JP2001178486-A.
 XX

PR 27-DEC-1999; 99JF-0371865.
 XX (CANO) CANON KK.
 XX WPI, 2001-592589/67.
 DR Microbial preparation of polyhydroxyalkanoic acids, using new carbon
 XX sources useful as raw material for biodegradable plastics -
 PT
 XX Disclousre; Page 9, 10pp; Japanese.
 PS
 XX The present invention relates to the production of
 CC polyhydroxyalkanoic acids. These can then be used in the production of
 CC biodegradable plastics. The present sequence is a Pseudomonas jessenii
 CC coding sequence described in the exemplification of the invention.
 XX
 SQ Sequence 1501 BP, 379 A; 339 C; 475 G; 308 T; 0 other;
 Query Match 76.1%; Score 1131; DB 22; Length 1501;
 Best Local Similarity 88.2%; Pred. No. 0;
 Matches 1299; Conservative 0; Mismatches 165; Indels 9; Gaps 6;

QY 13 TGAACGCTGGCGGAGGCTTAACACATGCAAGTCAGCGGTACAGGGAGCTTGCTCC 72
 Db 1 TGAACGCTGGCGGAGGCTT-MACACATGCAAGTCAGCGG-ATGACGGGAGCTTGCTCC 58
 QY 73 TGCTGACGAGCGGCGGACCGGGTGAAGCGTAGAATCTGCTAGTAGAGGGAGCA 132
 Db 59 TGAATTC-AGCGGCGGAGCGGGTGAAGTATGCTTAGAATCTGCTAGTAGAGGGAGCA 117
 QY 133 CATGTGMAACGATGTCTAATACCGCATACGCCCTGAGGGGMAAGAGGAGGACTCTTCG 192
 Db 118 CGTCTCGMAAGGAGCGCTAATACCGCATACGCTCTACGGGAGMAAGAGGAGG-CTTTC 175
 QY 193 GAGCCTTCGCTAATTAAGTAGAGCTGCGTAGAATTGCTAGTTGGTAGGGTAAAGGCTTA 252
 Db 176 GGGCTTCGCTAATTAAGTAGAGCTGCGTAGAATTGCTAGTTGGTAGGGTAAAGGCTTA 235
 QY 253 CCAAGGCGACGATCTTAATCTGATCTGAGAGATGACACAGTCACTGGGACTGAGACAC 312
 Db 226 CCAAGGCGACGATCCGTAATCTGATCTGAGAGATGACAGTCACTGGGACTGAGACAC 295
 QY 313 GAGCCAGACTCTTAAGGAGGACAGACAGTGGGAAATATTGACAAATGGGGCAAGCCTGAT 372
 Db 296 GGTCCAGACTCTTAAGGAGGACAGACAGTGGGAAATATTGACAAATGGGGCAAGCCTGAT 355
 QY 373 CCAGCCATGCGCGCTGTGTGAAGAGCCTTAGGGTTGTAAAGCACTTTCAGGGGTGAGG 432
 Db 356 CCAAGCATGCGCGCTGTGTGAAGAGCCTTAGGGTTGTAAAGCACTTTCAGGGGTGAGG 415
 QY 433 AAGGCTATAGATTAAATCGTTATCATCTTGACCTTACGCCCGGMAAGAGCACCGGCTAA 492
 Db 416 AAGGCTATTAACCTAAATACGTTAGTGTGACCTTACCGAGAAATTAAGCACCGGCTAA 475
 QY 493 CTCTGTGCGACAGCGCGGCTAATACAGAGGCTCAAGCTTATCGAATTACTGAGCG 552
 Db 476 CTCTGTGCGACAGCGCGGCTAATACAGAGGCTCAAGCTTATCGAATTACTGAGCG 535
 QY 553 TAAAGCGCGCTAGGTGTTTGTTAAGTCGAGTGTGAATCCAGGGCTCAACCTTGAA 612
 Db 536 TAAAGCGCGCTAGGTGTTTGTTAAGTGTGATGTGAACCCCGGCTCAACCTTGAA 595
 QY 613 TGGCACCGGATACCTGAGCTAGATAGTAGTAGAGGGGTGGAATTTCTGTGTAGAG 672
 Db 596 CTGCATTCAAACTGACAAAGCTAGATAGTAGTAGAGGGGTGGAATTTCTGTGTAGAG 655
 QY 673 GTGAATGCGTAGATATAGGAAGAACATCAGTGGCGAAGCGACACCTGATTAATAC 732
 Db 656 GTGAATGCGTAGATATAGGAAGAACACAGTGGCGAAGCGACACCTGATTAATAC 715
 QY 733 TGACACTGAGTGCAGAAAGCTGGGAGGACAAACAGATTGATACCTGTGTATCCAGCG 792
 Db 716 TGACACTGAGTGCAGAAAGCTGGGAGGACAAACAGATTGATACCTGTGTATCCAGCG 775

QY 793 CGTAAAGATGTCTACTAGACCCGTTGG--GTGTAAATGACTTAAGTGGCGGAGTAAAGCAA 850
 Db 776 CGTAAAGATGTAACTAGACCCGTTGGAGCCTTGAGCTTTAGTGGAGCTAAACGAT 835
 QY 851 TAAATGACCGCCTGGGAGTAGACCGCCGCAAGTTAAACTCAATGAATTACCGGGGC 910
 Db 836 TAAATGACCGCCTGGGAGTAGAGCGCCGCAAGTTAAACTCAATGAATTACCGGGGC 895
 QY 911 CCGCACAGCGGTGAGCATGTGTTTAATTGMAAGCAACGGGAAGAACTTACTACTC 970
 Db 896 CCGCACAGCGGTGAGCATGTGTTTAATTGMAAGCAACGGGAAGAACTTACTACTC 955
 QY 971 TTGACATCCACAGAACTTTGAGAGTCAAGTGTGCTCGGAGAACTGTGAGACAGGTG 1030
 Db 956 TTGACATCCACAACTTTCACAGATGATGAGTGTGCTCGGAGAACTGTGAGACAGGTG 1015
 QY 1031 CTGATGTGCTGTGTCAGCTCGTGTGTAATTTGGGTTAAGTCCCGTAACTGAGCGCA 1090
 Db 1016 CTGATGTGCTGTGTCAGCTCGTGTGTAATTTGGGTTAAGTCCCGTAACTGAGCGCA 1075
 QY 1091 ACCCTGTCTTATTGCGACACCGTAATGAGGGAACCTTAAGGAGACTGCCGCTGACA 1150
 Db 1076 ACCCTGTCTTATTGCGACACCGTAATGAGGGAACCTTAAGGAGACTGCCGCTGACA 1135
 QY 1151 AACCGAGAAAGGTGGGAGCAACGTCAAGTCAATCATGAGCCCTTAAGAGTGGGCTTACA 1210
 Db 1136 AACCGAGAAAGGTGGGAGTGAAGTCAATCATGAGCCCTTAAGAGTGGGCTTACA 1195
 QY 1211 CGTGTCAATAGGCGATTAACAGAGGCTTCAGAGCTAAGGATAGAGGAAATCCACAAA 1270
 Db 1196 CGTGTCAATAGGCGATTAACAGAGGCTTCAGAGCTAAGGATAGAGGAAATCCACAAA 1255
 QY 1271 GTACGTGTGATCGGATTTGAGTGTCAACTGCACTCCATGAGATCGAATCGTAGTA 1330
 Db 1256 ACGATGTGATCGGATTCGAGTGTGCAACTGCACTCCATGAGATCGAATCGTAGTA 1315
 QY 1331 ATGTGAATTAAGATGTCAACGTTGAATAGTTCCTGGGCTTGTACACACCGCCGTAC 1390
 Db 1316 ATGTGAATTAAGATGTCAACGTTGAATAGTTCCTGGGCTTGTACACACCGCCGTAC 1375
 QY 1391 ACCATGGAATGATGTGTCCAGAGTACAGTAAACCTTCGGGAGTGGCGGTTAC 1450
 Db 1376 ACCATGGAATGATGTGTCCAGAGTACAGTAAACCTTCGGGAGTGGCGGTTAC 1433
 QY 1451 ACCGAGTGTCAATGACTGGGTTGAAGTCTAC 1483
 Db 1434 ACCGAGTGTCAATGACTGGGTTGAAGTCTAC 1466

RESULT 4
 AAH77497
 ID AAH77497 standard, DNA, 1501 BP.
 XX
 XX AAH77497;
 XX
 XX 20-NOV-2001 (first entry)
 XX
 DE Pseudomonas jessenii P161 coding sequence fragment.
 XX
 KW Polyhydroxyalkanoate; PHA; ds.
 XX
 OS Pseudomonas jessenii.
 XX
 PV JP2001178485-A.
 XX
 XX 03-JUL-2001.
 PD
 XX 27-DEC-1999; 99JF-0371865.
 PF
 XX 27-DEC-1999; 99JF-0371865.
 PR
 XX (CANO) CANON KK.
 PA

XX WPI; 2001-586288/66.
 XX
 PT Production of a polyhydroxyalkanoate useful as a functional polymer -
 XX
 PS Disclosure, Page 9, 12pp; Japanese.
 XX
 CC The present invention describes a method of producing a
 CC polyhydroxyalkanoate (PHA) using a microbe. This may be *Pseudomonas*
 CC *cichorii* YN2, *Pseudomonas cichorii* H45 or *Pseudomonas jesseni* P161. The
 CC PHA produced using the method of the invention is useful as a functional
 CC polymer. The present sequence is a fragment of the P. jesseni coding
 CC sequence.
 XX
 SQ Sequence 1501 BP; 379 A; 339 C; 475 G; 308 T; 0 other;
 Query Match 76.1%; Score 1131; DB 22; Length 1501;
 Best Local Similarity 88.2%; Pred.No.0; Mismatches 165; Indels 9; Gaps 6;
 Matches 1299; Conservative 0;
 QY 13 TGAACGCTGGCGGCGAGCTTAAACACATGCAAGTCGAGCGGTAAACAGGGGAGCTTGCTCC 72
 Db 1 TGAACGCTGGCGGCGAGGCTTAAACACATGCAAGTCGAGCGG-ATGACGCGAGCTTGCTCC 58
 QY 73 TGTCTGACGAGCGCGGAGCGGTGAGTAAACGCGTAAAGTCTGCTAGTAGAGGGGACAA 132
 Db 59 TGAATTC-AGCGCGGAGCGGTGAGTAAATGCTTAAAGTCTGCTGAGTAGGGGACAA 117
 QY 133 CATGTGGAACGCAATCTATACCGCATACGCGCTGAGGGGAAAGAGGAGGACTTTCG 192
 Db 118 CGTCTGMAAAGGAGACGCTTAATCCGATACGTCCTACGAGGAAAGAGGAGG--CCTTC 175
 QY 193 GAGCCTTCGCTATTAGATGAGCCTGCGTGAATTAAGTCTAGTTGGTAGGGTAAAGGCTTA 252
 Db 176 GGGCCTTGCGCTATCGATGAGCCTGAGTCGAGTATGCTAGTTGGTAGGGTAAAGGCTTA 235
 QY 253 CCAAGGCGAGCATCTCTACCTGTCGAGAGGATGACAGTACACATCGGAGTACAGAC 312
 Db 236 CCAAGGCGAGCATCTCTACCTGTCGAGAGGATGACAGTACACATCGGAGTACAGAC 295
 QY 313 GGGCCAGACTCTCTACCGGAGGAGCAGAGTGGGGATATTGACAAATGGGCGCAGACTGAT 372
 Db 296 GGTCCAGACTCTCTACCGGAGGAGCAGAGTGGGGATATTGACAAATGGGCGCAGACTGAT 355
 QY 373 CCAAGCCTGCGGCTGTGGAAGAGGCTTAGGGTGTAAAGCATTTTCAGGGGTAGG 432
 Db 356 CCAAGCCTGCGGCTGTGGAAGAGGCTTAGGGTGTAAAGCATTTTCAGGGGTAGG 415
 QY 433 AAGGCTGATAGTTAATATGATATCTTGAAGTTCAGTCCCGAGAGAGCAGCGGCTAA 492
 Db 416 AAGGCTGATAGTTAATATGATATCTTGAAGTTCAGTCCCGAGAGAGCAGCGGCTAA 475
 QY 493 CTCTGTGCGAGCAGCGCGGTAAATACAGAGGCTGCAAGCGTTAATCGAATTACTGGAG 552
 Db 476 CTCTGTGCGAGCAGCGCGGTAAATACAGAGGCTGCAAGCGTTAATCGAATTACTGGAG 535
 QY 553 TAAAGGCGCGGTAGGTGTTTGTAGTGGATGGAATCCAGGGGCTCAACCTTGA 612
 Db 536 TAAAGGCGCGGTAGGTGTTTGTAGTGGATGGAATCCAGGGGCTCAACCTTGA 595
 QY 613 TGGACCCGATATCTGCTAGCTAGATATGATAGAGGGGTGGAATTTCTGTGTACG 672
 Db 596 CTGCTATCAAAATCTGACAGCTAGATATGATAGAGGGGTGGAATTTCTGTGTACG 655
 QY 673 GTGAATGCGTATGATATAGGAAGAACATGAGTGGCGAAGGAGACCTGAGATATAC 732
 Db 656 GTGAATGCGTATGATATAGGAAGAACACAGTGGCGAAGGAGACCTGAGATATAC 715
 QY 733 TGAACCTGAGTGGAGAGCGTGGGAGCAACAGATATTAGTACCTGTGATGCAAGC 792
 Db 716 TGAACCTGAGTGGAGAGCGTGGGAGCAACAGATATTAGTACCTGTGATGCAAGC 775
 QY 793 CGTAAACGATGTCTACTAGCCGTTGG--GTGTATGACTTAGTGGCGGACACTAACGCA 850

Db 776 CGTAAACGATGTCAACTAGCCGTTGGAGGCTTGAAGCTTATGAGTGGCGGACTTAAGCAT 835
 QY 851 TGAATGACCCGCTGGGAGATACGCGGAGGTTAAATCAATATATGAGCGGGGC 910
 Db 836 TGAATGACCCGCTGGGAGATACGCGGAGGTTAAATCAATATATGAGCGGGGC 895
 QY 911 CGGCAAGCGGTGAGCATGTGTTAATTCGAGAGCAGCGAAGACCTTACTACTC 970
 Db 896 CGGCAAGCGGTGAGCATGTGTTAATTCGAGAGCAGCGAAGACCTTACTACTC 955
 QY 971 TTGAATCAAGAAATTTAGAGATCAGATGTCCTTGGGAACTGTGAGCAGGT 1030
 Db 956 TTGAATCAAGAAATTTAGAGATCAGATGTCCTTGGGAACTGTGAGCAGGT 1015
 QY 1031 CTGATGCTGTCGTCAGCTGTCGTGTGGAATGTGGTTAAGTCCCGTAAGAGCGCA 1090
 Db 1016 CTGATGCTGTCGTCAGCTGTCGTGTGGAATGTGGTTAAGTCCCGTAAGAGCGCA 1075
 QY 1091 ACCCTTGCTCTTATTGCGACGACGTAAATGCTGGGAACTTTAAGAGACTGCCGTGACA 1150
 Db 1076 ACCCTTGCTCTTATTGCGACGACGTAAATGCTGGGAACTTTAAGAGACTGCCGTGACA 1135
 QY 1151 AACCGAGAGAGTGGGAGACGATCAAGTATGATGCGCTTACAGATAGGGCTACACA 1210
 Db 1136 AACCGAGAGAGTGGGAGACGATCAAGTATGATGCGCTTACAGATAGGGCTACACA 1195
 QY 1211 CGTGTACAAATGCGCTATACAGAGGCTGCAAGCTACAGATAGTGAACGATCCACAA 1270
 Db 1196 CGTGTACAAATGCGCTATACAGAGGCTGCAAGCTACAGATAGTGAACGATCCACAA 1255
 QY 1271 GTAGCTGTAATCGCGGATGAGATCTGACATCTGACATGAGTGGAAATGCTGTGTA 1330
 Db 1256 ACCGATGTAATCGCGGATGAGATCTGACATCTGACATGAGTGGAAATGCTGTGTA 1315
 QY 1331 ATCTGTAATCAAGATGTCAGGATACGTTCCCGGAGCTTGAACACACCGCCGTAC 1390
 Db 1316 ATCTGTAATCAAGATGTCAGGATACGTTCCCGGAGCTTGAACACACCGCCGTAC 1375
 QY 1391 ACCATGGAGTGTATGCTCCAGAGTACTAGCTTAAACCTTCGGGAGTGGGCTTACC 1450
 Db 1376 ACCATGGAGTGTATGCTCCAGAGTACTAGCTTAAACCTTCGGGAGTGGGCTTACC 1433
 QY 1451 ACGGAGTGTCAATGACTGAGGCTTGAAGTAC 1483
 Db 1434 ACGGAGTGTCAATGACTGAGGCTTGAAGTAC 1466
 RESULT 5
 ID AAS12097 standard; DNA; 1501 BP.
 XX AAS12097;
 AC
 XX
 DT 21-NOV-2001 (first entry)
 XX
 DE
 XX
 XX Pseudomonas jesseni 161 strain.
 KM Polyhydroxyalkanoate; alkanoate; microorganism; functional polymer; ds;
 KW medical material.
 OS Pseudomonas jesseni.
 XX
 PN EP1113033-A2.
 PD 04-UTL-2001.
 XX
 XX 22-DEC-2000; 2000EP-0128444.
 PF
 XX
 XX 27-DEC-1999; 99JP-0371863.
 PR 31-JAN-2000; 2000JP-0023078.
 PR 31-JAN-2000; 2000JP-0023080.
 PR 31-JAN-2000; 2000JP-0023083.

PR	30-MAR-2000; 2000JP-00955011.
PR	30-MAR-2000; 2000JP-00955012.
PR	30-MAR-2000; 2000JP-00955013.
PR	07-JUL-2000; 2000JP-0207089.
PR	07-JUL-2000; 2000JP-0207091.
PR	27-NOV-2000; 2000JP-0359789.
PA	(CANO) CANON KK.
PI	Honma T, Kobayashi T, Yano T, Kobayashi S, Imamura T, Suda S; Kamoku T;
XX	WPI; 2001-537748/60.
DR	
XX	
PT	New polyhydroxyalkanoates useful as functional polymers e.g. in medical devices
PS	
XX	Claim 36; Page 83-84; 184pp; English.
CC	The invention relates to polyhydroxyalkanoates comprising monomer units of diverse structures containing side chain substituents. This sequence CC represents a Pseudomonas jesseni 161 strain microorganism, capable of CC synthesising a polyhydroxyalkanoate from an alkanoate. By culturing a CC microorganism in a medium containing an alkanoate, a polyhydroxyalkanoat CC can be obtained. Polyhydroxyalkanoates are used as functional polymers, CC particularly in medical devices and materials. The use of microorganisms XX yields polymers of high purity and in high yield.
XX	
Sequence	1501 BP, 379 A, 339 C, 475 G, 308 T, 0 other;

	Query MarckS	76.1%	Score 1131;	DB 22;	Length 1501;	
	Best Local Similarity	88.2%	Pred. No. 0;			
	Matches 1299;	Conservative	0;	Mismatches 155;	Indels 9;	Gaps 6;
QY	13	TSAAACCTTGCGCGCAGGCTTAAACATATGCAATGTCGAGCGGTAAACAGGCGAGCTTGCTCC	72			
Db	1	TGACCCCTGCGCGCAGGCTTAAACATATGCAATGTCGAGCGGTAAACAGGCGAGCTTGCTCC	58			
QY	73	TGCTGACGACGCGCGGACGCGGTGAGTATCGGTGAGAAATCTGCCTGTAAGAGGCGGACAA	132			
Db	59	TGAATTC-AGCGCGCGGACCGGTGAGTATGCGCTGAGAAATCTGCCTGTAAGAGGCGGACAA	117			
QY	133	CATGTGAAAACGATGCTATATCCGCATATGCCCTTGAGGGGGAAAAGAGGGGACTCTTCC	192			
Db	118	CGCTGTGAAAAGGAGACGTATATCCGCATATCCCTTACGGAGAAACAGAGGGA--CCTTC	175			
QY	193	GAGCCTTCGCTATTAGATGAGCTGCGCTGAGATTAGCTAGTTGATAGGTTAAAGGCTTA	252			
Db	176	GCGCCTTGCGCTATGAGATGAGCTGAGCTGAGTTAGCTAGTTGATAGGTTAAAGGCTTA	235			
QY	253	CGAAGGCGAGATCTCTCTAATCTGCTGTGAGAGAAAGACATGACACTGAGACTGAGACAC	312			
Db	236	CGAAGGCGAGATCTCTCTAATCTGCTGTGAGAGAAAGATGATGACACTGAGACTGAGACAC	295			
QY	313	GCGCCAGACTCTCTACCGGAGGACGACAGTGGGAAATATTGACAATGGGCGCAAGCCTGAT	372			
Db	296	GCGTCCAGACTCTCTACCGGAGGACGACAGTGGGAAATATTGACAATGGGCGCAAGCCTGAT	355			
QY	373	CGACGCATGCGCGGTGTGTGAGAAAGGCTTAAGGTTGTAAGACCTTCAGGGGTGAGAG	432			
Db	356	CGACGCATGCGCGGTGTGTGAGAAAGGCTTCCTCGATTGTAAAGCACTTTAAGTTGGAGAG	415			
QY	433	AAGGCGTATGAGTTAATACGTTATCATCTTGACCTTGACCCCGAAGAAAGACCGGCTAA	492			
Db	416	AAGGCGATTTAACCTAATATGCTATGCTGTTTGAACGTTACCGACGAATATAGCACCGGCTTA	475			
QY	493	CTCTGTGCAGACGACCGCGGTATATCAAGAGGTCGAAGCGTTATCGAATTCTGAGCG	552			
Db	476	CTCTGTGCAGACGACCGCGGTATATCAAGAGGTCGAAGCGTTATCGAATTCTGAGCG	535			
QY	553	TAAAGGCGCGGTGAGTGTGTTGTGTAATCGATGTGAATCCAGAGGCTTCAACTTTGAA	612			
Db	536	TAAAGGCGCGGTGAGTGTGTTGTGTAATCGATGTGAATCCAGAGGCTTCAACTTTGAA	595			

OY		613	TGACACCAGATCTGGTAGTCAAGATAGTGAGAGGGGTGGAATTTCCTGTATACG	672
Db		596	CTGCATCCAAACTGACAAGCTAAGTAAGTATGAGAGGGGTGGAATTTCCTGTATACG	655
OY		673	GTEGAATGCGTATGATATGGAAGAACATCATGTGGCGAAGCGCACCTTGGACTATAC	732
Db		656	GTEGAATGCGTATGATATGGAAGAACACCATGTGGCGAAGCGCACCTTGGACTATAC	715
OY		733	TGACACTAGAGTGCAGAAAGCTGAGGAGCAAACAGGANTAGATACCTGTAGTCCAGC	792
Db		716	TGACACTAGAGTGCAGAAAGCTGAGGAGCAAACAGGATTAGATACCTGTAGTCCAGC	775
OY		793	CGTAAACGATGTCTATGACCCGTTGG--GTTGTATGACTTATGTGGCGAGCTAACGCAA	850
Db		776	CGTAAACGATGTCTATGACCCGTTGGAGCCCTTGACCTCTTATGTGGCGAGCTAACGCA	835
OY		851	TAAATGAGACCGGCTGGGGAGTACGGGCCGAGGCTTTAAACTCAATAATGATGAGGGGGC	910
Db		836	TAAATGAGACCGGCTGGGGAGTACGGGCCGAGGCTTTAAACTCAATAATGATGAGGGGGC	895
OY		911	CCGCAACAGCGGTGAGAGCATGTGTTTTATTCGAGCAAACGGCAAGAACCTTACTACTC	970
Db		896	CCGCAACAGCGGTGAGAGCATGTGTTTTATTCGAGCAAACGGCAAGAACCTTACTACTC	955
OY		971	TTGACATCCACAGAACATTTAGAGATCABAATGTCCTCTGGGAACTGTGAGAAGSTG	1030
Db		956	TTGACATCCACAGAACATTTCCAGAGATGAGATGAGTCTCTGGGAACTTTGAGAAGSTG	1015
OY		1031	CTGECATGCGTGTGCTCACTCGTGTGTGAAATGTTGGGTTAAAGTCCCGTAAACGAGCGCA	1090
Db		1016	CTGECATGCGTGTGCTCACTCGTGTGTGAGATGTTGGGTTAAAGTCCCGTAAACGAGCGCA	1075
OY		1091	ACCCCTTGCTCTTATTTGCGACAGCTAAATGCTGTGGGAACCTTATGAGAGATGCGCGTGACA	1150
Db		1076	ACCCCTTGCTCTTATTTGACACAGACGTAAATGCTGTGGGAACCTTATGAGAGATGCGCGTGACA	1135
OY		1151	AACCGAGAGAGTGTGGGACACAGCTCAAGTCATATGCGCTTACGAGTAAAGGGCTTACACA	1210
Db		1136	AACCGAGAGAGTGTGGGATGAGCTCAAGTCATATGCGCTTACGAGCTTAAAGGGCTTACACA	1195
OY		1211	CGTGCTACATAGGGCTATACAGAGGGCTGCAGACTAGCGATAGAGCAATCCCAACAA	1270
Db		1196	CGTGCTACATAGTGTGGTACAGAGGGGTGGCAAGCCGACAGGTGAGAGCTTAACTCCACAA	1255
OY		1271	GTAAGTCGTAAGCCGAGTTGAGTCTCAACTCGACTCATGATGAGTCCGAAATCCGTAGTA	1330
Db		1256	AACGATCGTAAGTCCGAGTCCGAGTCCGAACTCGACTCATGATGAGTCCGAAATCCGTAGTA	1315
OY		1331	ATGTGTAATCAGATATGTACAGCTGTAATAGTTCCCGGCGCTTGTATACACCGCCCTGTAC	1390
Db		1316	ATGTGTAATCAGAAATGTGCGGTAATAGTTCGCGGCGCTTGTATACACCGCCCTGTAC	1375
OY		1391	ACCATGGAGTGTGATTGCTCCAGAAAGTAGTACTTAAACCTTCCGGGAGTGGCGGTATAC	1450
Db		1376	ACCATGGAGTGTGATTGCTCCAGAAAGTAGTACTTAAAC--TTCCGGGAGAGCGGTATAC	1433
OY		1451	ACGAGTGTCAATGACTGAGGCTTGAAGCTTAC	1483
Db		1434	ACGAGTGTCAATGACTGAGGCTTGAAGCTTAC	1466
RESULT 6:				
ID	AA164177	standard; DNA; 1501 BP.		
XX	AA164177;			
XX	26-FEB-2002	(first entry)		
DE	Pseudomonas jessenii strain p161	16S rRNA gene sequence.		
KM	16S rRNA gene; strain p161; polyhydroxyalkanoate; alkylaryl group;			

KM alkanoate polymerisation; microbial enzyme; glass transition temperature;
 KW adhesive; identification; ribosomal RNA; de.
 OS *Pseudomonas jessenii*.
 PN EP118629-A2.
 XX
 XX 25-JUL-2001.
 PD
 PF 27-DEC-2000; 2000EP-0128540.
 XX
 XX 27-DEC-1999; 99UP-0371864.
 PR 27-DEC-1999; 99UP-0371867.
 PR 27-DEC-1999; 99UP-0371868.
 PR 27-DEC-1999; 99UP-0371869.
 PR 31-JAN-2000; 2000UP-0023024.
 PR 31-JAN-2000; 2000UP-0023025.
 PR 28-NOV-2000; 2000UP-0361323.
 XX
 XX (CANO) CANON KK.
 PA
 PI Honma T, Kobayashi T, Yano T, Kobayashi S, Imamura T, Suda S;
 PI kenmoku T;
 DR WPI, 2001-598513/68.
 XX
 XX Polyhydroxyalkanoate comprises monomeric unit that has pendant
 PT alkylaryl group, optionally substituted on benzene ring.
 XX
 XX Disclosure; Fig 12; 95pp; English.
 PS
 XX The present sequence represents that of the 16S rRNA (ribosomal RNA) gene
 CC from *Pseudomonas jessenii* strain 161. Prior to the present invention,
 CC strain 161 had not been assigned to a particular species; comparison
 CC of the strain 161 16S rRNA gene DNA with 16S rRNA gene sequences of
 CC known micro-organisms of the genus *Pseudomonas* identified 161 as a
 CC strain of *Pseudomonas jessenii*. The specification describes a
 CC polyhydroxyalkanoate comprising one or more monomeric units that have
 CC pendant alkylaryl groups, optionally substituted on the benzene ring.
 CC The specification also describes a process of producing the
 CC polyhydroxyalkanoate by culturing a micro-organism in a medium containing
 CC a raw material alkanoate and a yeast extract so that the alkanoate is
 CC polymerised. The invention is used for the production of novel
 CC polyalkanoates using microbial enzymes. The polymer is adhesive at
 CC ambient temperatures and, when mixed with other polymers, reduces the
 CC glass transition temperature of the blend. Orientation and crystallinity
 CC can be tailored by changing the pendant substituent groups. The desired
 CC polymer can be obtained without interference from unintended monomer
 CC units.
 CC
 XX
 XX Sequence 1501 BP; 379 A; 339 C; 475 G; 308 T; 0 other;
 SQ
 Query Match 76.1%; Score 1131; DB 23; Length 1501;
 Best Local Similarity 88.2%; Pred. No. 0;
 Matches 1289; Conservative 0; Mismatches 165; Indels 9; Gaps 6;

Db 226 CCAAGGAGACATCCGTACCTGCTGAGAGATGATCACTGACATCGAATCGAAGCAC 295
 Qy 313 GGGCCAGACTCTTACGGGAGGACAGCACTGGGGAAATTTGACAAATGGCGCCAGCCTGAT 372
 Db 296 GGTCCAGACTCTTACGGGAGGACAGCACTGGGGAAATTTGACAAATGGCGCCAGCCTGAT 355
 Qy 373 CCAGCCATGCGCGCTGTGTGAGAGAGGCTTAGGGTGTGTAAGACATTTGAGGGGTGAG 432
 Db 356 CCAAGCAATGCGCGCTGTGTGAGAGAGGCTTAGGGTGTGTAAGACATTTGAGGGGTGAG 415
 Qy 433 AAGGGTATGATTAAATACGTTATCATCTTGACGTTAGCCCAAGAAAGACCGGCTTA 492
 Db 416 AAGGGCAATTAACTTAATACGTTAGTTGTTGAGGTTAACCAAGAAATTAAGCACCGGCTTA 475
 Qy 493 CTCGTGTCAGACACCGCGGTAATACAGAGGGTGCAGAGCTTAATGGAATTTACTGAGGCG 552
 Db 476 CTCGTGTCAGACACCGCGGTAATACAGAGGGTGCAGAGCTTAATGGAATTTACTGAGGCG 535
 Qy 553 TAAAGCGCGCTAGGTTGTTTAACTCGATGTGAAATCCAGGAGCTCAACCTTGAA 612
 Db 536 TAAAGCGCGCTAGGTTGTTTAACTCGATGTGAAATCCAGGAGCTCAACCTTGAA 595
 Qy 613 TGGCACCCGATACCTGGCTAGCTAGATGATGTAAGGGGTGTGGAATTTCTGTGTAGCG 672
 Db 536 CTGCAATTAACCTGACAGCTAGATGATGTAAGGGGTGTGGAATTTCTGTGTAGCG 655
 Qy 673 GTGAATATCGTAGATATAGAGAGGACATGATGCGCAAGGCGACACCTGACTAATAC 732
 Db 656 GTGAATATCGTAGATATAGAGAGGACATGATGCGCAAGGCGACACCTGACTAATAC 715
 Qy 733 TGACACTAGGTGCGAAAGCGTGGGGAGCAAAACGATTAATACCTGTGTAGTCAACGC 792
 Db 716 TGACACTAGGTGCGAAAGCGTGGGGAGCAAAACGATTAATACCTGTGTAGTCAACGC 775
 Qy 793 CGTAAGAGTGTACTAGACCGTTGG--GTTGTATGACTTAGTGGGCGAGCTAGCGAA 850
 Db 776 CGTAAGAGTGTACTAGACCGTTGG--GTTGTATGACTTAGTGGGCGAGCTAGCGAA 835
 Qy 851 TAAGTAGACCGCTGGGAGATACCGCGCAAGGTTAAATCTCAATGATTAAGCGGGGC 910
 Db 836 TAAGTAGACCGCTGGGAGATACCGCGCAAGGTTAAATCTCAATGATTAAGCGGGGC 895
 Qy 911 CCGCAAGCGGTGAGACATGTTGTTAATTCAGAGCAAGCAAGCACTTACCTAATC 970
 Db 896 CCGCAAGCGGTGAGACATGTTGTTAATTCAGAGCAAGCAAGCACTTACCTAATC 955
 Qy 971 TTGACATCCACAGAACTTTGAGAGATCAGATGATGCTTGGGAACTGTGAGACAGGTG 1030
 Db 956 TTGACATCCATGAACCTTCCAGAGATGAGATGGGTGCTTGGGAACTTTGAGACAGGTG 1015
 Qy 1031 CTGCATGGCTGTCTGACAGCTGTGTGTGAATGTTGGGTTAAGTCCCGTAAGACGCGA 1090
 Db 1016 CTGCATGGCTGTCTGACAGCTGTGTGTGAATGTTGGGTTAAGTCCCGTAAGACGCGA 1075
 Qy 1091 ACCCTTGCTTTATTTGACAGACGTAATGATGGGAACTTTAAGAGACTGCGGTGACA 1150
 Db 1076 ACCCTTGCTTTATTTGACAGACGTAATGATGGGAACTTTAAGAGACTGCGGTGACA 1135
 Qy 1151 AACCGAGAAAGTGGGAGCAGCTCAATGATCATGAGCCCTTAACGATGAGGCTACACA 1210
 Db 1136 AACCGAGAAAGTGGGAGTGAACCTCAAGTATCATGAGCCCTTAACGATGAGGCTACACA 1195
 Qy 1211 CGTGCTAATAGGGGTATACAGAGGGGTGCAAGCTAGCATGATGAGCGAATCCCAAAA 1270
 Db 1196 CGTGCTAATAGGGGTATACAGAGGGGTGCAAGCTAGCATGATGAGCGAATCCCAAAA 1255
 Qy 1271 GTAGCTGTAGTCCGATTTGAGAGTGTGCAACTGACCTCATGAAATGCGATGCTTAGTA 1330
 Db 1256 ACCGATGTAGTCCGATTTGAGAGTGTGCAACTGACCTCATGAAATGCGATGCTTAGTA 1315
 Qy 1331 ATCGGATGTAGATGTCACGCTGAATAGCTTCCCGGCGCTTTTACACACCGCGCGTAC 1390

Dh 1316 ATCCGAAATCAGAAATGTGCGCGTGAATACGTTCCCGGCGCTTGACACACCGCCGCTCAC 1375
Qy 1391 ACCATGGAGATGATTTGCTCCAGAAAGTACGTTAACCTTCGGGAGATGGCGTTACC 1450
Db 1376 ACCAAGGAGAGTGGTTGACACAGAGTACGTTACCTTCCGAGAGACGTTACC 1433
Qy 1451 ACGAGTGTCAATGACTGCGGGTTGAAGTCTAC 1483
Db 1434 ACGTGTATTCATGACTGCGGGTGAAGTCTAC 1466

RESULT 7

AA139554
ID AA139554 standard; DNA; 1501 BP.

AA139554;
XX

05-SEP-2002 (first entry)
Dt

Pseudomonas jessenii Pl61 strain DNA.
De

Polyhydroxyalkanoate; PHA; benzoyl alkanolic acid; device material;
Km

water repellent; medical material; Pseudomonas jessenii; Pl61 strain; ds.
Xx

Pseudomonas jessenii.
Xx

EP118782-A2.
Pn

20-MAR-2002.
Pd

14-SEP-2001; 2001EP-0122101.
Pf

14-SEP-2000; 2000JP-0279900.
Pr

13-DEC-2000; 2000JP-0378827.
Pr

31-MAY-2001; 2001JP-0165238.
Pr

31-MAY-2001; 2001JP-0165509.
Pr

11-SEP-2001; 2001JP-0275063.
Pr

(CANO) CANON KK.
Pa

Honna T, Sugawa E, Yano T, Imamura T, Kennoku T;
Pi

WPI; 2002-481356/52.
Dr

New polyhydroxyalkanoate useful as device material, water repellent
Pt

material, and medical material.
Ps

Disclosure; Page 57; 75pp; English.
Pp

The invention relates to a novel method for manufacturing
Cc

polyhydroxyalkanoate (PHA) comprising preparing a medium containing a
Cc

substituted benzoyl alkanolic acid, and culturing a microorganism capable
Cc

of synthesizing the PHA using the substituted benzoyl alkanolic acid in
Cc

the medium. The method also includes the extraction and recovery of PHA
Cc

from the bacteria culture. PHA is useful as a device material, water
Cc

repellent material, and a medical material. This polynucleotide sequence
Cc

represents the DNA of Pseudomonas jessenii Pl61 strain relating to the
Cc

invention.
Cc

NOTE: This polynucleotide sequence is shown in the sequence listing,
Cc

however it is not further described in the specification.
Cc

Sequence 1501 BP; 379 A; 339 C; 475 G; 308 T; 0 other;
Sq

Query Match 76.1%; Score 1131; DB 24; Length 1501;
Best Local Similarity 88.2%; Pred. No. 0; Mismatches 165; Indels 9; Gaps 6;
Matches 1299; Conservative 0; Mismatches 165; Indels 9; Gaps 6;

Dh 59 TGAATTC-AGCGGGGAGCGGGTGAATATGATTCCTAGGAATCTGCTGTAGTGGGGACAA 117
Qy 133 CATGTGAAACGATGCTTAATACCGCATACGCCCTTACAGGGGAGAAAGAGGAGACTTTCG 192
Db 118 CGTTCGAAAGGAGACGCTTAATACCGCATACGCCCTTACAGGGGAGAAAGAGGAGACTTTCG 175
Qy 193 GAGCCTTCGCTTATGATGAGCCCTGAGATTAAGTATGAGTGTAGAGGTAAAGGCTTA 252
Db 176 GGGCTTGGCTTATGATGAGCCCTGAGATTAAGTATGAGTGTAGAGGTAAAGGCTTA 235

Qy 253 CCAAGGCGAGATCTCTAATGCTGTGAGAGATGACCACTGACACTGGAGCTTGAACAC 312
Db 236 CCAAGGCGAGATCTCTAATGCTGTGAGAGATGACCACTGACACTGGAGCTTGAACAC 295

Qy 313 GAGCCAGACTCTACAGGAG 372
Db 296 GGTCCAGACTCTACAGGAG 355

Qy 373 CCAAGCAG 432
Db 356 CCAAGCAG 415

Qy 433 AAGGCTATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 492
Db 416 AAGGCTATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 475

Qy 493 CTCTGTGCGCAG 552
Db 476 CTCTGTGCGCAG 535

Qy 553 TAAAGCGCGGTAGT 612
Db 536 TAAAGCGCGGTAGT 595

Qy 613 TGACACCGGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 672
Db 596 CTGCTATCAAACTGACCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATG 655

Qy 673 GTGAATGCTGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 732
Db 656 GTGAATGCTGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 715

Qy 733 TGAACATGAGTGTGAAAGCGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 792
Db 716 TGAACATGAGTGTGAAAGCGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 775

Qy 793 CGTAAAGATGCTACTAGCCGTTGG-GTGTATGACTTATGATGATGATGATGATGATGAT 850
Db 776 CGTAAAGATGCTACTAGCCGTTGGAGGCTTGAAGCTTATGATGATGATGATGATGATGAT 835

Qy 851 TAAATTAACCGCTGGGAGATGAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 910
Db 836 TAAATTAACCGCTGGGAGATGAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 895

Qy 911 CCGCAG 970
Db 896 CCGCAG 955

Qy 971 TTGACATCCACAGAAACATTGAGAGATCAGATGATGATGATGATGATGATGATGATGATG 1030
Db 956 TTGACATCCACAGAAACATTGAGAGATCAGATGATGATGATGATGATGATGATGATGATG 1015

Qy 1031 CTGATGAGTGTGCTAGCTCGT 1090
Db 1016 CTGATGAGTGTGCTAGCTCGT 1075

Qy 1091 ACCCTTGTCTTATTTGCGACAGCTGATGATGATGATGATGATGATGATGATGATGATG 1150
Db 1076 ACCCTTGTCTTATTTGCGACAGCTGATGATGATGATGATGATGATGATGATGATGATG 1135

Qy 1151 AACCGAG 1210
Db 1136 AACCGAG 1195

QY 1091 ACCCTTGCTTATTTGCGACAGCTAATGGTGGAACTTTAAGAGACTGCCGTGACA 1150
 Db 1076 ACCCTTGCTTATTTGCGACAGCTAATGGTGGAACTTTAAGAGACTGCCGTGACA 1135
 QY 1151 AACCGAGAGAGTGGGGACGACGTCAAGTCAATGAGCCCTTACGAGTAGGGCTACACA 1210
 Db 1136 AACCGAGAGAGTGGGGACGACGTCAAGTCAATGAGCCCTTACGAGTAGGGCTACACA 1195
 QY 1211 CGTGCTACAAATGGCGCTATPACAGAGGGCTGCAAGCTAGAGTAGAGACGAAATCCACAAA 1270
 Db 1196 CGTGCTACAAATGGCGCTATPACAGAGGGCTGCAAGCTAGAGTAGAGACGAAATCCACAAA 1255
 QY 1271 GTACGTCTAGTCCGAGATTGAGTGTGCAATGCACTTCACTGAAGTGGAAATCGTAGTA 1330
 Db 1256 ACCGATCGTAGTCCGAGATTGAGTGTGCAATGCACTTCACTGAAGTGGAAATCGTAGTA 1315
 QY 1331 ATCGTGAATCAGAAATGTCAAGGTGAATCGTTCCCGGGCTTTGACACACCGCCGTCAC 1390
 Db 1316 ATCGGGAATCAGAAATGTCAAGGTGAATCGTTCCCGGGCTTTGACACACCGCCGTCAC 1375
 QY 1391 ACCATGAGAGTGAATTTGCTCCAGAAAGTAGTAGCTTAACCTTGCGGGATGGCGTTACG 1450
 Db 1376 ACCATGAGAGTGAATTTGCTCCAGAAAGTAGTAGCTTAACCTTGCGGGATGGCGTTACG 1433
 QY 1451 ACGGAGTGTCAATGACTGGGGTGTGAAGTCTAC 1483
 Db 1434 ACGGTGTGATCATGACTGGGGTGTGAAGTCTAC 1466

RESULT 9
 AAI66302
 ID AAI66302 standard; DNA; 1501 BP.
 AC AAI66302;
 XX
 DT 22-JAN-2002 (first entry)
 XX
 DE Pseudomonas jessenii coding sequence.
 XX
 KW Polyhydroxyalkanoate; 3-hydroxyphenylalkanoic acid; PHA;
 XX medical material; biodegradable polymer; ds.
 OS Pseudomonas jessenii.
 XX
 EN EPI130043-A2.
 XX
 PD 05-SEP-2001.
 XX
 PF 28-FEB-2001; 2001EP-0104922.
 XX
 PR 29-FEB-2000; 2000JP-0054317.
 XX
 PR 29-FEB-2000; 2000JP-0054667.
 XX
 PA (CANO) CANON KK.
 XX
 PI Honma T, Yano T, Kobayashi S, Imamura T, Kermoku T, Kozaki S;
 XX
 DR WPI; 2002-012494/02.
 XX
 PT Novel polyhydroxy alkanates containing 3-hydroxy phenyl alkanolic acid
 XX monomer units for use as biodegradable and functional polymers -
 PS
 XX Disclosure; Page 32-33; 46pp; English.
 CC The present invention relates to polyhydroxy alkanates (PHA) containing
 CC 3-hydroxy phenyl alkanolic acid monomer units. These can be used as
 CC biodegradable, bio-compatible, functional polymers, as device material
 CC and as soft medical material. The present sequence is a coding sequence
 CC from Pseudomonas jessenii.
 XX
 SQ Sequence 1501 BP; 379 A; 339 C; 475 G; 308 T; 0 other;

Query Match 76.1%; Score 1131; DB 24; Length 1501;
 Best Local Similarity 88.2%; Pred. No. 0;
 Matches 1299; Conservative 0; Mismatches 165; Indels 9; Gaps 6;

QY 13 TGAACGCTGGCGGAGGCTTAAACATGCAAGTCAAGCGGTAAACAGGGAGCTTCTCC 72
 Db 1 TGAACGCTGGCGGAGGCTTAAACATGCAAGTCAAGCGGTAAACAGGGAGCTTCTCC 58
 QY 73 TGCTGACAGAGGCGGAGCGGTGAGTAAACCGTAGAATCTGCTAGTAGAGGGGACAA 132
 Db 59 TGAATTC-AGCGGCGAGCGGTGAGTAAACCGTAGAATCTGCTAGTAGAGGGGACAA 117
 QY 133 CATGTGAAAACGCAATGCTAATACCGCATACGCCCTAGAGGGGAAAAGAGGGGACCTTGG 192
 Db 118 CGTCTGAAAAGGAGCGCTAATACCGCATACGCTCTACGGGAGAAACAGGGGAC--CCTTC 175
 QY 193 GAGCTTCCGCTATTAGATAGCCCTGCGTAGATTAGCTAGTTGGTGAAGGCTTA 252
 Db 176 GGGCTTGGCGTAAACAGATAGCCCTAGTCCGATTAGCTAGTTGGTGAAGGCTTA 235
 QY 253 CCAAGCGAGCATCTTAATCTGGTCTGAGAGTAGACAGTCACTAGGAGTGAAGAC 312
 Db 236 CCAAGCGAGCATCTTAATCTGGTCTGAGAGTAGTCACTCACTGAACTGAAGAC 295
 QY 313 GGGCCAACTCTTACGGGAGGACAGAGTGGGGAAATTTGACAAATGGCGCAAGCTGAT 372
 Db 296 GGTCCAACTCTTACGGGAGGACAGAGTGGGGAAATTTGACAAATGGCGCAAGCTGAT 355
 QY 373 CCAGCCATGCGCGGTGTGTAAAGAGGCGCTTGAAGCGCTTCAAGGGTAGAG 432
 Db 356 CCAGCCATGCGCGGTGTGTAAAGAGGCTTGAAGCGCTTCAAGGGTAGAG 415
 QY 433 AAGGGTATAGTTAATACCTTATCATCTTGAAGTCCCGAAGAAACACCGGCTAA 492
 Db 416 AAGGGATTAACCTAATACCTTATCATCTTGAAGTCCCGAAGAAACACCGGCTAA 475
 QY 493 CTCTGTCCAGACCGCGCGCTTATACAGAGGTCAGAGGTAAATCGAAATTAACGGGCG 552
 Db 476 CTCTGTCCAGACCGCGCGCTTATACAGAGGTCAGAGGTAAATCGAAATTAACGGGCG 535
 QY 553 TAAAGCCCGGTAGTGTGTTGTTAGTGGATGTGAATCCAGGGCTCAACTTGGAA 612
 Db 536 TAAAGCCCGGTAGTGTGTTGTTAGTGGATGTGAATCCAGGGCTCAACTTGGAA 595
 QY 613 TGGCAACCGATCTGCTAGCTAGATAGTAAAGAGGGTGTGGAATTCCTGTAGCG 672
 Db 596 CTGCATTCAAACTGACAACTAGAGTATGTAAAGGGTGTGGAATTCCTGTAGCG 655
 QY 673 GTGAATGCGTAGATTAAGAAAGAACATCAGTGGCGAAGCGCAACCTGACTAATAC 732
 Db 656 GTGAATGCGTAGATTAAGAAAGAACATCAGTGGCGAAGCGCAACCTGACTAATAC 715
 QY 733 TGACACTGAGGTGCGAAAGCTGGGGAGCAAAACAGATTAGTACCCTGTGATCGAGC 792
 Db 716 TGACACTGAGGTGCGAAAGCTGGGGAGCAAAACAGATTAGTACCCTGTGATCGAGC 775
 QY 793 CGTAAAGATGTCTAATAGCCGTTGG--CTTGTAAATGATTTAGTGGCGAGCTAACGCA 850
 Db 776 CGTAAAGATGTCTAATAGCCGTTGG--CTTGTAAATGATTTAGTGGCGAGCTAACGCA 835
 QY 851 TAACTAGACCGCTGGGAGATACGCGCGCAAGCTTAACTCAATGAATGACGGGGGC 910
 Db 836 TAACTAGACCGCTGGGAGATACGCGCGCAAGCTTAACTCAATGAATGACGGGGGC 895
 QY 911 CCGGACAAGGGTGGAGCATGTGCTTAAATGAGAGCAACGGGAAGAACTTAACCTACTC 970
 Db 896 CCGGACAAGGGTGGAGCATGTGCTTAAATGAGAGCAACGGGAAGAACTTAACCAAGCC 955
 QY 971 TTGACATCCACAGAACATTTGAGAGATGAGTGTGCTTCCGGAACCTGTGAGACAGGTG 1030
 Db 956 TTGACATCCACAGAACATTTGAGAGATGAGTGTGCTTCCGGAACCTGTGAGACAGGTG 1015
 QY 1031 CTGATGAGCTGTGCTAGCTCGTGTGTGAATGTTGGTTAGTCCGTAAACAGCGCA 1090

Chr	Start	End	Strand	Gene	Transcript	Feature	Score	Length	GC	GC3	GC35	GC34	GC33	GC32	GC31	GC30	GC29	GC28	GC27	GC26	GC25	GC24	GC23	GC22	GC21	GC20	GC19	GC18	GC17	GC16	GC15	GC14	GC13	GC12	GC11	GC10	GC9	GC8	GC7	GC6	GC5	GC4	GC3	GC2	GC1	GC0	GC-1	GC-2	GC-3	GC-4	GC-5	GC-6	GC-7	GC-8	GC-9	GC-10	GC-11	GC-12	GC-13	GC-14	GC-15	GC-16	GC-17	GC-18	GC-19	GC-20	GC-21	GC-22	GC-23	GC-24	GC-25	GC-26	GC-27	GC-28	GC-29	GC-30	GC-31	GC-32	GC-33	GC-34	GC-35	GC-36	GC-37	GC-38	GC-39	GC-40	GC-41	GC-42	GC-43	GC-44	GC-45	GC-46	GC-47	GC-48	GC-49	GC-50	GC-51	GC-52	GC-53	GC-54	GC-55	GC-56	GC-57	GC-58	GC-59	GC-60	GC-61	GC-62	GC-63	GC-64	GC-65	GC-66	GC-67	GC-68	GC-69	GC-70	GC-71	GC-72	GC-73	GC-74	GC-75	GC-76	GC-77	GC-78	GC-79	GC-80	GC-81	GC-82	GC-83	GC-84	GC-85	GC-86	GC-87	GC-88	GC-89	GC-90	GC-91	GC-92	GC-93	GC-94	GC-95	GC-96	GC-97	GC-98	GC-99	GC-100	GC-101	GC-102	GC-103	GC-104	GC-105	GC-106	GC-107	GC-108	GC-109	GC-110	GC-111	GC-112	GC-113	GC-114	GC-115	GC-116	GC-117	GC-118	GC-119	GC-120	GC-121	GC-122	GC-123	GC-124	GC-125	GC-126	GC-127	GC-128	GC-129	GC-130	GC-131	GC-132	GC-133	GC-134	GC-135	GC-136	GC-137	GC-138	GC-139	GC-140	GC-141	GC-142	GC-143	GC-144	GC-145	GC-146	GC-147	GC-148	GC-149	GC-150	GC-151	GC-152	GC-153	GC-154	GC-155	GC-156	GC-157	GC-158	GC-159	GC-160	GC-161	GC-162	GC-163	GC-164	GC-165	GC-166	GC-167	GC-168	GC-169	GC-170	GC-171	GC-172	GC-173	GC-174	GC-175	GC-176	GC-177	GC-178	GC-179	GC-180	GC-181	GC-182	GC-183	GC-184	GC-185	GC-186	GC-187	GC-188	GC-189	GC-190	GC-191	GC-192	GC-193	GC-194	GC-195	GC-196	GC-197	GC-198	GC-199	GC-200	GC-201	GC-202	GC-203	GC-204	GC-205	GC-206	GC-207	GC-208	GC-209	GC-210	GC-211	GC-212	GC-213	GC-214	GC-215	GC-216	GC-217	GC-218	GC-219	GC-220	GC-221	GC-222	GC-223	GC-224	GC-225	GC-226	GC-227	GC-228	GC-229	GC-230	GC-231	GC-232	GC-233	GC-234	GC-235	GC-236	GC-237	GC-238	GC-239	GC-240	GC-241	GC-242	GC-243	GC-244	GC-245	GC-246	GC-247	GC-248	GC-249	GC-250	GC-251	GC-252	GC-253	GC-254	GC-255	GC-256	GC-257	GC-258	GC-259	GC-260	GC-261	GC-262	GC-263	GC-264	GC-265	GC-266	GC-267	GC-268	GC-269	GC-270	GC-271	GC-272	GC-273	GC-274	GC-275	GC-276	GC-277	GC-278	GC-279	GC-280	GC-281	GC-282	GC-283	GC-284	GC-285	GC-286	GC-287	GC-288	GC-289	GC-290	GC-291	GC-292	GC-293	GC-294	GC-295	GC-296	GC-297	GC-298	GC-299	GC-300	GC-301	GC-302	GC-303	GC-304	GC-305	GC-306	GC-307	GC-308	GC-309	GC-310	GC-311	GC-312	GC-313	GC-314	GC-315	GC-316	GC-317	GC-318	GC-319	GC-320	GC-321	GC-322	GC-323	GC-324	GC-325	GC-326	GC-327	GC-328	GC-329	GC-330	GC-331	GC-332	GC-333	GC-334	GC-335	GC-336	GC-337	GC-338	GC-339	GC-340	GC-341	GC-342	GC-343	GC-344	GC-345	GC-346	GC-347	GC-348	GC-349	GC-350	GC-351	GC-352	GC-353	GC-354	GC-355	GC-356	GC-357	GC-358	GC-359	GC-360	GC-361	GC-362	GC-363	GC-364	GC-365	GC-366	GC-367	GC-368	GC-369	GC-370	GC-371	GC-372	GC-373	GC-374	GC-375	GC-376	GC-377	GC-378	GC-379	GC-380	GC-381	GC-382	GC-383	GC-384	GC-3
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FT	misc_difference <td>1511</td> <td>/note=<td>"bases 1500-1511 are identified as 'n'"</td></td>	1511	/note= <td>"bases 1500-1511 are identified as 'n'"</td>	"bases 1500-1511 are identified as 'n'"
XX	US5508193-A.			
XX	16-APR-1996.			
XX	31-AUG-1993;	93US-0114695.		
XX	31-AUG-1993;	93US-0114695.		
XX	(MINT) UNTV MINNESOTA.			
XX	Mandelbaum RT, Wackelt LP;			
XX	WPI; 1996-208726/21.			
XX	Biologically pure culture of atrazine-degrading <i>Pseudomonas</i> - useful to detoxify atrazine, e.g. in soil, at a wide variety of concns.			
XX	Example 2; Column 31-34; 34p; English.			
XX	Novel bacterial strain ADP (ATCC 55464), isolated from atrazine-contaminated soil, is capable of degrading s-triazine cpds., including atrazine. In an attempt to identify the strain, the 16S ribosomal RNA sequence (AAT18760) was compared to that of <i>Escherichia coli</i> (AAT18759), <i>Pseudomonas citromellolis</i> ATCC 13674 (AAT18761-63), <i>Pseudomonas aeruginosa</i> (AAT18764), <i>Pseudomonas testosteroni</i> (AAT18765) and <i>Pseudomonas cepacia</i> (AAT18766). It was concluded that ADP is closely related to, but distinct from, <i>P. citromellolis</i> and <i>P. aeruginosa</i> .			
XX	Sequence 1518 BP; 380 A; 335 C; 470 G; 300 U; 33 other;			
XX	Query Match	74.8%; Score 1111; DB 17; Length 1518;		
XX	Best Local Similarity	69.1%; Pred. No. 0;		
XX	Matches 1024; Conservative 258; Mismatches 191; Indels 9; Gaps 6			
QY	3 TAGCTCAGATTAAAGCTGTGGCGGAGGCTTAAACACATGCAATGCAGCGGTACAGGG	62		
DB	20 UGGCUCAGAUAGAGCGUCGCGCGAGGCCUACACAGUCAGAGUCGACGGG-AUGAAGG	78		
QY	63 AGCTTGCTCTGCTGACGAGCGGCGAGCGGCTGATGACGCGTGAAGATCTTGCTGATG	122		
DB	79 AGCUCGUCUCUGAUAUC-AGCGGCGAGCGGUGAUAUAGCUCAGAGAUUCUCUGAUAUG	137		
QY	123 AGGGGACACAACTGAGAAACGATGTTATACCGCATAGCCCTGAGGGGAGAAAGAGG	182		
DB	138 UGGGGAGUAGGUCGCGAAGAGGGCGCUAUAACGCAUACGUCUGAGGAGAAAGGGG	197		
QY	183 GGACTCTTGGAGGCTTCGCTTATAGATAGAGCTTCGCTGAGATTAGCTGTTGGTAGG	242		
DB	198 GGAUUCU--CGGACCTUCACGCUAUCNAGUAGGCUUAGGUCGUAUUGAGUUGGUGGGG	255		
QY	243 TAAAGGCTTACCAAGAGGAGATCTCAATGTGCTGAGAGATGACAGTACACTGGG	302		
DB	256 UAAAGGCUACCAAGGCGAGCAUCCUUAUCUGGUCUAGAGAGCAUCCAGUCACACUGA	315		
QY	303 ACTGAGACAGGCCCAAGCTTCTACGSGAGGACAGCAGTGGGAGATATTGGAACATGGCG	362		
DB	316 ACUGAGACAGGUCACAGUCUACGCGGAGGACAGCAGUGGCGAUAUUGGACAUAGGCGG	375		
QY	363 CAAGCTCATCCAGCAATGCGCGGTGTGTAAGAAGGCTTACGGGTGTAAGCACTTTC	422		
DB	376 AAAGCTCAUCCAGCCCAUCCGCGGUGUGAAGAGAGUCCUCGGAUUGUAAAGCACUUA	435		

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QY 423 AGGGGTGAGGAGGATGATAGGTTATATACCTTATCATCTTACGTTAGCCCAAGAGAG 482
DB 436 AGUGGGAGAGAGGAGGAGUAUAUUAUACUUGUCUGUACGUAUACCAAGAAUAG 495
QY 483 CACCGGCTAACTCTGTGCGACGACGCCGCTAATACAGAGGTGCAACGTTAATCGAA 542
DB 496 CACCGGUAACUUCGUCGACGACGCCGUAUAUAGAAAGGUGGACGCUAAUAVCGAA 555
QY 543 TTACTGGGCGTAAAGGCGCGTACGCTGTTTGTATAGTCGATGTGAATCCCGAGCTC 602
DB 556 UUAUUGGGCUAAAGGCGCGGUAUUGGUAUUAUAGAAAGAAACAGUGGCGAAGCGACCTU 615
QY 603 AACCTTGATGACGACCCGATCTGCGCTAGCTAGTATGATAGAGGGGTGGAATTTTC 662
DB 616 AACUGGGAAUCUGAUCNNAAACUAUAGAGCUAAGAGUACGGAGAGGGUGUGGAUUTUC 675
QY 663 CTGTGTAGCGGTGAAAATGCGTATGATATAGGAAGAAATCATGATGCGAAGCGACACCT 722
DB 676 CUGUGUAGCGGUAUUGGUAUUAUAGAAAGAAACAGUGGCGAAGCGACACCTU 735
QY 723 GGAATAATCTGACATGAGGTGCGAAAGCGTGGGAGAGAAACAGATTAGATACCTTGG 782
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QY 783 TACTCCACGCGCTAAACGATGTCTACTAGCCGTTGGTTT--GTAATGACTTAGTGGCGCA 840
DB 796 UAUUCCACGCGCTAAACGATGTCTACTAGCCGTTGGTTT--GTAATGACTTAGTGGCGCA 855
QY 841 GCTACGCAATATAGTACCGGCTGGGAGTACCGGCGGAGTTAAACCTCAATATAT 900
DB 856 GCUAACGCGAUAUAGUGUACCGGCGUUGGAGUACGCGCGAGUUAUAAACCAUAGUAAU 915
QY 901 TGAAGGGGGCGGCAACAGCGGTGAGCATGTGTATTATTCAGAACCGAGAAACC 960
DB 916 UGACGGGGGCGGCAACAGCGGTGAGCATGTGTATTATTCAGAACCGAGAAACC 975
QY 961 TTACTACTCTTGACATCCACAGAAATTTGAGATACAGATGTGCTTGGGAACTGT 1020
DB 976 UUAUUGGCGGUAUAGUGUAGAACUUAUCCAGAAUAGUAGUUGGCGUUGGAGAAUUA 1035
QY 1021 GAGACAGGTGCTGATGCTGTCTGATGCTGCTGTTGTAATGTTGGTAAATCCCGT 1080
DB 1036 GACACAGGTGCTGATGCTGTCTGATGCTGCTGTTGTAATGTTGGTAAATCCCGT 1095
QY 1081 AAGGAGCGCAACCTTGTCTTATTTGCCAGACGTAATGTGTGGAACTTTAAGAGACT 1140
DB 1096 AAGGAGCGCAACCTTGTCTTATTTGCCAGACGTAATGTGTGGAACTTTAAGAGACT 1154
QY 1141 GCGGTGACAAACCGGAGAGAGTGGGAGCAGCTCAATGATGAGCCCTTTCAGATA 1200
DB 1155 GCGGTGACAAACCGGAGAGAGTGGGAGUAGCAGUACUAGUAGCCUUAUAGCGGCA 1214
QY 1201 GGGCTACACAGCTGCTACAAATGCGTAAACAGAGGCTGCAAGCTAGCATAGTACGA 1260
DB 1215 GGGCTACACAGCTGCTACAAATGCGTAAACAGAGGCTGCAAGCTAGCATAGTACGA 1274
QY 1261 ATCCCAAGAAAGTACGTCGATGCGGATTTGAGTGTGCAATTCGACTCAATGAGTGGGA 1320
DB 1275 AUCCCAAGAAAGTACGTCGATGCGGATTTGAGTGTGCAATTCGACTCAATGAGTGGGA 1334
QY 1321 ATGCTAGTATGCTGATGATCAGATATGCAACGCTGATGATGCTTCCGCGGCTTTCACAC 1380
DB 1335 AUGCTUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 1394
QY 1381 CGCGCGTACACATGAGGAGTGTGATTTGCTCCAGAAAGTACGTTAATCCCTTGGGGAT 1440
DB 1395 CGCGCGTACACATGAGGAGTGTGATTTGCTCCAGAAAGTACGTTAATCCCTTGGGGAT 1452
QY 1441 GGGCGTTACACGAGAGTGTCAATGACTGGGGTTTGAAGTCTA 1482
DB 1453 GACGCTUACACGAGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 1494

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RESULT 15
AA511023
ID AA511023 standard, DNA, 1467 BP.
AC AA511023;
XX
AC AA511023;
XX
DT 24-OCT-2001 (first entry)
XX
DE Pseudomonas aeruginosa 16S ribosomal RNA gene.
XX
KM Antisense; bacterial 16S ribosomal RNA; rRNA; bacterial infection;
XX human; food grain supplement; livestock; poultry; therapeutic; ds.
XX Pseudomonas aeruginosa.
XX
PN MO200142457-A2.
XX
PD 14-JUN-2001.
XX
PF 29-NOV-2000; 2000MO-US42391.
XX
PR 29-NOV-1999; 99US-0168150.
XX
PA (AVTB-) AVI BIOPHARMA INC.
XX
PI Iversen PL;
XX
DR WPI; 2001-457295/49.
XX
PT Antibacterial compound, useful for treating bacterial infections and as
PT livestock and poultry food supplement, comprises antisense
PT oligonucleotides complementary to bacterial 16S and 23S rRNA -
XX
PS Disclosure; Page - : 62pp; English.
XX
XX
AA511021-AA511034 represent the coding sequences of bacterial 16S
CC ribosomal RNA (rRNA) genes. The sequences were used to design anti-
CC bacterial compounds comprising substantially unchanged antisense
CC oligomers containing 8-40 nucleotide subunits, including a targeting
CC nucleic acid sequence at least 10 nucleotides in length which is
CC complementary to a bacterial 16S or 23S rRNA nucleic acid sequence.
CC The antisense oligomers are used for treating a bacterial infection
CC in a human or a mammalian animal produced by Escherichia coli, Salmonella
CC typhimurium, Pseudomonas aeruginosa, Vibrio cholera, Neisseria
CC gonorrhoea, Helicobacter pylori, Bartonella henselae, Haemophilus
CC influenza, Shigella dysenteriae, Staphylococcus aureus, Mycobacterium
CC tuberculosis, Streptococcus pneumoniae, Treponema pallidum and Chlamydia
CC trachomatis. The antibacterial compound may be used as a food grain
CC supplement in livestock and poultry food composition.
CC Note: The present sequence is not shown in the specification but has
CC been accessed from Genbank using the appropriate accession number given
CC in the specification.
XX
SQ Sequence 1467 BP; 370 A; 330 C; 458 G; 309 T; 0 other;
XX
Query Match 74.0%; Score 1100.2; DB 22; Length 1467;
Best Local Similarity 88.2%; Pred. No. 0;
Matches 121; Conservative 0; Mismatches 158; Indels 6; Gaps 3;
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QY 141 AAGCGATGCTAATCCGATACGCTGAGAGGGGAAAGAGGGGACCTTCGAGGCTTC 200
DB 86 AAGCGATGCTAATCCGATACGCTGAGAGGGGAAAGAGGGGACCTTCGAGGCTTC 143
QY 201 CGCTATTAGATGAGCCTGCGTGAAGTATGATGATGATGATGATGATGATGATGATGATGAT 260
DB 144 CGCTATTAGATGAGCCTGCGTGAAGTATGATGATGATGATGATGATGATGATGATGATGAT 203
QY 261 AGATCTTAACTGTGCTGAGAGATGACAGTCACTAGGACTGAGACACGCGCCACA 320

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Db 204 ACGATCCGTAACGTGCTGAGAGATGATCAGTCACACTGGAATGAGACACGGCTCAGA 263
Qy 321 CTCCACGGGAGGAGCAGGTGGGAAATTGACAAATGGGCGCAAGCTTGATCAACCT 380
Db 264 CTCCTACGGGAGGAGCAGGTGGGAAATTGACAAATGGGCGCAAGCTTGATCAACCT 323
Qy 381 GCCCGGTGTGAGAAAGGACCTTAGGGTTGAAAGCACTTACAGGGGTGAGAAAGGAGTA 440
Db 324 GCCCGGTGTGAGAAAGGACCTTAGGGTTGAAAGCACTTAAAGTTGGAGAAAGGACAT 383
Qy 441 TAGGTTAATACGTTATCATCTTGAAGTGAAGCCCGAGAAAGCAACGGCTAACTGTGAC 500
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Qy 561 GCGTAGGTGTTTGTAAAGTGAAGTGAATCCAGGGCTCAACCTTGAAATGGCACCC 620
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Qy 1399 AGTTGATTGCTCCAGAAAGTACGTTAACTTGGGGATGCGGTTACACGAGATG 1458
Db 1344 AGTGGGTTGCTCCAGAAAGTACGTTAACTTGGGGG--GACGGTTACACGAGAGT 1401
Qy 1459 GTCATGACTGGGGT 1473
Db 1402 ATTCAATGACTGGGGT 1416

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Search completed: January 30, 2004, 19:20:09
Job time : 443.94 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 30, 2004, 18:26:40 : Search time 3491.17 Seconds
(without alignments)
10345.086 Million cell updates/sec

Title: US-09-737-297-1
Perfect score: 1486
Sequence: 1 gttagctcagatcgacgct.....ctgggggtcgagcttcacgcg 1486

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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2: em_esthum:*
3: em_estin:*
4: em_estma:*
5: em_estov:*
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25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrt:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	815.2	54.9	6499	28	BH771024
2	615.6	41.4	1084	29	BZ439740
3	605	40.7	1053	29	BZ447500
4	598.6	40.3	1010	29	BZ431523

5	594	40.0	1079	28	BH705272	BH705272	BOMK47TF
6	591.4	39.8	1044	29	BZ463550	BZ463550	BOMK96TF
7	591.4	39.8	1051	29	BZ494182	BZ494182	BOMK98TF
8	590.4	39.7	1016	29	BZ426201	BZ426201	BOMK28TF
9	589.8	39.7	1031	28	BH656222	BH656222	BOMK28TF
10	588.6	39.6	741	14	CD042372	CD042372	psHB040XF
11	587.8	39.6	1077	29	BZ450751	BZ450751	BOMK63TF
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13	571.6	38.5	1054	28	BH647750	BH647750	BOMK13TF
14	566.2	38.1	974	29	BZ440868	BZ440868	BOMK51TF
15	557.2	37.5	1069	29	BZ474941	BZ474941	BOMK59TF
16	553.8	37.3	699	14	CD043647	CD043647	psHB005XK
17	552.6	37.2	1106	29	BZ469058	BZ469058	BOMK54TF
18	550.8	37.1	951	28	BH651765	BH651765	BOMK30TF
19	549.4	37.0	641	14	CD040169	CD040169	psHB032XK
20	548.2	36.9	1068	29	BZ576668	BZ576668	msH2_5045
21	542	36.5	901	29	BZ461852	BZ461852	BOMK01TF
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23	538.4	36.2	977	29	BZ459292	BZ459292	BOMK028TF
24	535.6	36.0	918	29	BZ437960	BZ437960	BOMK072TF
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26	528	35.5	1143	28	BH814866	BH814866	PRPC15_Ma
27	526.2	35.4	995	28	BH700021	BH700021	BOMK021TF
28	524.8	35.3	905	29	BZ572385	BZ572385	msH2_2610
29	524.2	35.3	1033	29	BZ561605	BZ561605	pacS2_164
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32	513.2	34.5	873	28	BH705306	BH705306	BOMK08TF
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34	511.6	34.4	882	28	BH486252	BH486252	BOMK19TF
35	511.4	34.4	837	28	BZ483676	BZ483676	BOMK16TF
36	510.8	34.4	862	28	BH527452	BH527452	BOMK16TF
37	508.8	34.2	846	28	BH562180	BH562180	BOMK28TF
38	507.8	34.2	835	28	BH552149	BH552149	BOMK28TF
39	507.6	34.2	1036	28	BZ502068	BZ502068	BOMK125TF
40	506.8	34.1	604	10	BE204135	BE204135	EST396811
41	504.8	34.0	848	28	BH730827	BH730827	BOMK156TF
42	504.8	34.0	857	28	BH730853	BH730853	BOMK024TF
43	504.6	34.0	831	29	BZ501502	BZ501502	BOMK057TF
44	502.4	33.8	1082	29	BZ459110	BZ459110	BOMK059TF
45	500.2	33.7	848	28	BH535640	BH535640	BOMK194TF

ALIGNMENTS

RESULT 1
LOCUS BH771024 6499 bp DNA linear GSS 01-MAY-2002
DEFINITION LMGtag746 MG1363 Random Sequence Tag Library Lactococcus lactis
SUBSP. cremoris genomic, genomic survey sequence.
VERSION BH771024
ACCESSION BH771024
KEYWORDS GI:203733981
SOURCE
ORGANISM
Lactococcus lactis subsp. cremoris
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Lactococcus

REFERENCE
AUTHORS Bolotin, A., Ehrlich, S.D. and Sorokin, A.
TITLE Studies of genomes of dairy bacteria Lactococcus lactis
JOURNAL Sci. Aliments, (2002) In press
COMMENT Contact: Sorokin A
Genetique Microbienne

INRA
CRJ INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France
Tel: 33 1 34 65 25 16
Fax: 33 1 34 65 25 21
Email: sorokine@jouy.inra.fr
best homologues in strain IL1403 is ywGA (78%)
Class: shocgun
High quality sequence start: 30
High quality sequence stop: 6471.

FEATURES
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 Location/Qualifiers
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 /clone_lib="MG1363 Random Sequence Tag Library"
 /note="Vector: pSGM02; Site 1: SmaI; Library of
 chromosomal fragments of L.lactis strain MG1363 was
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 BASE COUNT 1946 a 1228 c 1683 g 1642 t
 ORIGIN

Query Match 54.9%; Score 815.2; DB 28; Length 6499;
 Best Local Similarity 76.4%; Pred. No. 1e-229;
 Matches 1132; Conservative 0; Mismatches 333; Indels 17; Gaps 10;

QY 3 TAGCTCAGATTGAACTGCGCGGCGGCTTAAACACATGCAAGTGCAGCGGT-AAACAGG 61
 DB 544 TGGCTCAGACGAACTGCGCGGCGGCTTAAACATGCAAGTGCAGCGGT-AAACAGG 602
 QY 62 GAGCTTCTCC-TGCTGACGAGCGGCGGCGGCTTAAACATGCAAGTGCAGCGGT-AAACAGG 119
 DB 603 GTGCTTGCACCAATTGAAAGACGCAACGCGGTGAGTAAACGCGGCGGCGGCGGCTT 662
 QY 120 TAGAGGGGACCAATGTCGAAACGCGGTGAGTAAACGCGGTGAGTAAACGCGGTGAGT 178
 DB 663 GAGCGGGGACCAATGTCGAAACGCGGTGAGTAAACGCGGTGAGTAAACGCGGTGAGT 722
 QY 179 -GAGGGGACTCTTGGAGCTTCCGCTATTAGATGAGCTGCGGTGAGTAAACGCGGT 234
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 QY 235 TGGTAGGGTAAAGGCGCTACCAAGGCGGCGGCTTAAACATGCAAGTGCAGCGGT-AAACAGG 294
 DB 783 TGGTAGGGTAAAGGCGCTACCAAGGCGGCGGCTTAAACATGCAAGTGCAGCGGT-AAACAGG 842
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 DB 843 ACATTGGGACTGACACGCGGCGGCGGCTTAAACATGCAAGTGCAGCGGT-AAACAGG 902
 QY 355 AATGGGCGGCGGCTTAAACATGCAAGTGCAGCGGT-AAACAGG 414
 DB 903 AATGGGCGGCGGCTTAAACATGCAAGTGCAGCGGT-AAACAGG 962
 QY 415 GCACTTTCAGGGGCTGACGAGGCGGTAAACATGCAAGTGCAGCGGT-AAACAGG 473
 DB 963 ACTCTGTTGTTAGAGAAACGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1022
 QY 474 CAGAGAGACGCGGCTTAAACATGCAAGTGCAGCGGT-AAACAGG 533
 DB 1023 CCCGAAAGGAGCGGCTTAAACATGCAAGTGCAGCGGT-AAACAGG 1082
 QY 534 TAATCGGAATTAATGCGGCTTAAACATGCAAGTGCAGCGGT-AAACAGG 593
 DB 1083 TGTCCGATTTATTTGGCGCTTAAACATGCAAGTGCAGCGGT-AAACAGG 1142
 QY 594 CAGAGGCTCAACTTGAATGCAACCGGATCTGCTTAAACATGCAAGTGCAGCGGT-AAACAGG 653
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QY 832 AGTGGCGACCTTAAGCAATTAAGTACCCGCTTGGGAGTACGCGCGGCAAGTTAAACT 891
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 QY 892 CAATGAATTAAGCGGCGGCGCGGCAAGCGGTGAGTGGTTTAAATGCAAGCAAG 951
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 DB 1252 AGTGAAGCAATCCCAAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1311
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 QY 1860 GAAGTGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1919
 DB 1372 TGTACACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1431
 QY 1920 TGTACACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1473
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 DB

RESULT 2
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 DEFINITION genomic survey sequence.
 ACCESSION BZ439740
 VERSION BZ439740.1 GI:26695676
 KEYWORDS GSS.
 SOURCE Brassica oleracea
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eucolecyledons; core eucolec; rosids
 ; eucosids II; Brassicales; Brassicaceae; Brassica.
 REFERENCE 1 (bases 1 to 1084)
 AUTHORS Town,C.D., Van Aken,S., Uteback,T., Koo,H. and Frazer,C.M.
 TITLE Whole genome shotgun sequencing of Brassica oleracea
 JOURNAL Unpublished
 COMMENT Other GSSs: BONDUS4TR
 CONTACT: Chris Town
 TIGR 712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TF
 Class: sheared ends.
 Location/Qualifiers

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total DNA inserted into pHD51 using BstXI linkers"
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ORIGIN
Query Match      41.4%; Score 615.6; DB 29; Length 1084;
Best Local Similarity 75.8%; Pred. No. 5.5e-171;
Matches 825; Conservative 0; Mismatches 234; Indels 29; Gaps 4;

QY 250 CTACCAAGCGCAGCATCTCTACTGCTGCTGAGAGATGACCACTGCACTGGAGCTGAGA 309
DB 3 CTACCAAGCGCAGCATCTCTACTGCTGCTGAGAGAGATGACCACTGCACTGGAGCTGAGA 61
QY 310 CACGAGCCGAGACTCTCTACGGAGGAGCAGATGGAGAAATTTGAGCAATGGGGCAAGCCT 369
DB 62 CACGAGCCGAGACTCTCTACGGAGGAGCAGATGGAGAAATTTTCCGCAATGGGGCAAGCCT 121
QY 370 GATCCAGCATGCCGCGTGTGTGAAGAAGCCTTAGCGTTGTAAGCACTTTCAGGGGTG 429
DB 122 GACGAGCAATGCCGCGTGTGTGAAGAAGCCTTAGCGGTCTGAACTTCTTTTCCAGAG 181
QY 430 AGGAAGGTGATAGGTTAATACGTATCATCTTGAGCTTAAGCCCGAGAAAGACCCGCG 489
DB 182 AAGAA-----CAATGACGATATCTGGGAAATTAAGCATCGCG 218
QY 490 TAACTCTGTGCAGACCGCGGTATATACAGAGGGTGAAGCCTTATCGAATTAATCG 549
DB 219 TAACTCTGTGCAGACCGCGGTATATACAGAGGATGAAGCAAGCTTATCGAATTAATCG 278
QY 550 GCGTAAAGCGCGCTAGTGTGTTGTTAATCGAGTGTGAATCCAGAGGCTCAACCTTG 609
DB 279 GCGTAAAGCGCTAGTGTGTTGTTAATCGAGTGTGAATCCAGAGGCTCAACCTTG 338
QY 610 GAATGGACCCGATCTGCTAGCTAGATAGATGATGAGAGGGGTGTGAATTTCCGTGTA 669
DB 339 GACAGCGGTGTGAAGCTTACCAAGTTAGATGATGAGAGGGAGAGAAATTTCCGATGA 398
QY 670 GCGGTGAATGCGTGAATATAGAGAGACATAGTGGCGAAGCGCACCTGTGACTTAA 729
DB 399 GCGGTGAATGCGTGAATATAGAGAGACATAGTGGCGAAGCGCACCTGTGACTTAA 458
QY 730 TACTGACACTGAGGTGGAGAAAGCGTGGGAGCAAAAGGATTAGATACCTGTGTGCTCA 789
DB 459 CACTGACACTGAGAGAGAAAGCTTGGGAGCGAATGGGATTAGATACCTGTGTGCTCT 518
QY 790 CGCGGTAAAGCATGTCTACTAGCCGTTG---GGTGTGAATGACTTATAGTGGCGCACTAC 846
DB 519 AGCGGTAAAGCATGTCTACTAGCCGTTG---GGTGTGAATGACTTATAGTGGCGCACTAC 578
QY 847 GCATATAGTGAACCGCTGGGAGTACAGGCCCGCAAGGTTAACTCAATGATTTGACGG 906
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DB 639 GGGCCCGCACAAGCGGTGAGAGACTGTGTTAATTTGAAAGCAACGCGAAGAACTTACT 698
QY 967 ACTTTGACATCCACAGAAATTTGAGAGATCGATGATGTCCTTGGGAACTGTGAGACA 1026
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QY 1027 GGTCTGCAATGGCTGTGCTGAGCTGCTGTGTAATGTTGGTTAAGTCCCGTATAGCG 1086
DB 759 GGTGTGCAATGGCTGTGCTGAGCTGCTGTGTAATGTTGGTTAAGTCCCGTATAGCG 818
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DB 819 CGCAACCTGTCTCTTATTGCGCA--CGTTGAGTTTGAACCTTGAACAGACTCGCGT 876
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DB 877 GATTAAGCCGAGAGAGAGTGAAGTATGATGATGATGATGATGATGATGATGATGATGATG 936
QY 1207 CACACGTGCTACATAGCGCTGATACAGAGGGCTGCAAGCTAGAGATGATGAGGAATCCCA 1266
DB 937 CACACGTGCTACATAGCGCGGAGCAAGAGGTGCGCATCCCGAGAGGTGATGATGATGAT 996
QY 1267 CAAAGTACGTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1326
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DB 1057 AGTATATCG 1064

RESULT 3
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DEFINITION BONKRF40TR BO_1.6_2_KB tot Brassica oleracea genomic clone BONKRF40,
ACCESSION BZ447500
VERSION BZ447500.1 GI:26712943
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SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eucosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE Town,C.D., Van Aken,S., Uteirack,T., Koo,H. and Fraser,C.M.
whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished
COMMENT Other GSSs: BONKRF40TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq Primer: TR
Class: sheared ends.
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/mol_type="genomic DNA"
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total DNA inserted into pHD51 using BstXI linkers"
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Query Match      40.7%; Score 605; DB 29; Length 1053;
Best Local Similarity 75.5%; Pred. No. 7.5e-168;
Matches 815; Conservative 0; Mismatches 235; Indels 29; Gaps 4;

QY 212 GAGCTGCGTGAATTAAGTCTAGTGTGTAAGGTTAAAGGCTTACCAAGGCGAGATCTCTAA 271
DB 1053 GAGCTGCGTGTGATTAAGTCTAGTGTGTAAGGTTAAAGGCTTACCAAGGCGAGATCTCTAA 994
QY 272 CTGCTGAGAGAGATGACAGTCACTGAGGAGCTAGACAAGGCGCAGACTCTTACAGGGA 331
DB 993 CTGCTGAGAGAGATGATAGCCACTGAGACTAGACAGGCGCAGACTCTTACAGGGA 934
QY 332 GGCAGAGATGGGGAATTTGAGCAATGGCGCAAGCTGATTCAGCAGCATGCCGCTGTGT 391

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Db	933	CGACGACGTGGGGAAAT-TTCCGCATGTGGGCGAAAGCCTGACGGAGCAATCCCGCGTGAG	875
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Db	874	GTGAAAGGCGCTACGGGTCTCTGAACCTCTTTTCCAGAGAAAGAG-----	831
Qy	452	GTATCATCTTGACGTTAGCCCCCAAGAACACACCGGCTAACCTGTGGCAGACGCCG	511
Db	830	-----CATGACCGGTACTCTGGGGAATAGCATCGGCTAACTGTGCCAGACGCCG	778
Qy	512	GTAAATCAGAGGCTGACCAAGCTTAATCGGAATTACTGCGCTAAAGCCGCGTAGTGCT	571
Db	777	GTATATCAGAGGATGACAGCGTTATCCCGGAATGATTGGCGTAAAGCGTCTGTAAGTGCG	718
Qy	572	TTGTTTAGTCGGATGTGAAATCCCAAGGCGCTAACCTTGGAATGGCACCCGATACGGCTA	631
Db	717	TTTTTAAATCCCGCTCAATCCCAAGGCGCTAACCCCTGACACGCGGTGAAACTACCA	658
Qy	632	GCTAAGATGTGTAAGGAGGGGTGGAATTTCTGTGTATGACGCTGAATGCGTAGATAG	691
Db	657	GCTTAGTACGGTAAGGGGACAGAGGGAATTTCCGGGTGAGCGGTGAATGCGTAGATAG	598
Qy	692	GAAGAAACATCACTGCGCAAGCGCACACCTCTGACTTAATCTGACACTAGAGTGGCAAG	751
Db	597	GAAGAAGACCAACACCGCGGAACCACTGCTGCGGCCGACACTGACCTGAGACCAAG	538
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Qy	929	ATGTGTTTAATTCGAGCAACGCGAAGAACCTTACCTACTTTGACATCCACAGAACT	988
Db	357	ATGTGTTTAATTCGATGCAAGCAAGCAAACTTACCAAGGGCTTGACATCCGCGAATCC	298
Qy	989	TTTAGAGATCAATGTGCTTCCTCGGGAATCTGTGACAGAGTGTCTGATGGCTGTCTGAG	1044
Db	297	TCTTGAAGAAGAGGGGTGCTTCGAGAAACGCGACACAGGTGTGACATGCTGTCTCG	238
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LOCUS			
BZ431523 1010 bp DNA linear GSS 13-DEC-2007			
ACCESSION			
BZ431523			
VERSION			
BZ431523.1 GI:26677909			
KEYWORDS			
GSS.			
SOURCE			
Brassica oleracea			

ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Brassicica oleracea	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta, eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.	1 (bases 1 to 1010)	Town,C.D., Van Aken,S., Uteback,T., Koo,H. and Fraser,C.M.	Whole genome shotgun sequencing of Brassica oleracea	Unpublished
Other GSSs: BONHD81TR	Contact: Chris Town	TIIG	9712 Medical Center Drive, Rockville, MD 20850, USA.	Tel: 301-838-3523	Fax: 301-838-0208
Email: cdtown@ictgr.org	DNA is from a doubled haploid provided by Tom Osborn.	Seq primer: TP	Class: end.	Location/Qualifiers	
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			/note="Vector: pHOSt; Site: 1: BstXI; 1.6-2 kb sheared total DNA inserted into pHOSt using BstXI linkers"		
BASE COUNT	192 a	327 c	236 g	255 t	
ORIGIN					
Query Match	40.3%;	Score 598.6;	DB 29;	Length 1010;	
Best Local Similarity	76.1%;	Pred. No. 5.8e-166;			
Matches 788;	Conservative	0;	Mismatches 219;	Indels 28;	Gaps 3
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DB	1010	GATTACTCTGTTGGTAGGGTTAAAGGCTTACCAAGCGACAGATCTTCACTGAGTCTGAG	951		
OY	284	GATGACCAATGCACTGAGGACTGAGACACAGCGCCAGCTCTTACCGGAGGACAGTGGG	343		
DB	950	GATGATGACCAATGCACTGAGGACTGAGACACAGCGCCAGCTCTTACCGGAGGACAGTGGG	891		
OY	344	GATTATGACATATGGGCGCAAGCCTGATCCAGCAGCCGCGTGGTGAAGAAGCCCTT	403		
DB	890	GATTATGACATATGGGCGCAAGCCTGATCCAGCAGCCGCGTGGTGAAGAAGCCCTT	831		
OY	404	AGGATTGTAAACACTTTTCAGGGGTGAGGAAGGGTGTATAGTTAATACGTTATCATCTTG	463		
DB	830	CGGGTCTGTAATCTTTTCCGAGGAAGAAG-----CAATG	794		
OY	464	ACGTTAGCCCCGAGGAAGACACCGGCTTACCTTGTGACACAGCCCGGTTATATCAGAG	523		
DB	793	ACGTTAGCCCCGAGGAAGACACCGGCTTACCTTGTGACACAGCCCGGTTATATCAGAG	734		
OY	524	GTGCAAGCCTTATCGGAATTAAGGCGGTAAAGCGCGCTAGTGGTGTGTTGTTAACTCG	583		
DB	733	ATGCAAGCCTTATCGGAATTAAGGCGGTAAAGCGCGCTAGTGGTGTGTTGTTAACTCG	674		
OY	584	ATGTGAATCCCAAGGCTTCAACCTTGGATGCGCAACCCGATATCTGGCTAGTAAAGTATGG	643		
DB	673	CCGTCAAAATCCCAAGGCTTCAACCTTGGATGCGCAACCCGATATCTGGCTAGTAAAGTATGG	614		
OY	644	TAGAGGGGTGTGAATTTTCCGTGTGAGGGGTGAATCGATAGATATATAGAGGAAATATCA	703		
DB	613	TAGAGGGGTGTGAATTTTCCGTGTGAGGGGTGAATCGATAGATATATAGAGGAAATATCA	554		
OY	704	GTGCGAAGCGCAACCTTGAATTAATCTGACATGAGGTGCGAAAGCTGGGGAGCA	763		
DB	553	ACGGCAAAAGCACTGTGTTGGGCGGACATGACATGAGAGGAAAGCTTGGGGAGCGA	494		
OY	764	ACGAGTTTGAATACCTGTATGTGTCACGCGGTAAAGATGTCACTAGACGTTG---GGT	820		

Db 493 ATGGATTAGATACCCCGAGTCTCTACCCGTAACATGATCTAGCGCTGTGCGTA 434
 QY 821 TGTAAATGACTAGTGGCCAGCTAACCGCATATAGTAGACCGCTGGGAGTACGCGCGA 880
 Db 433 TCGACCCGTCAGTCTCTAGCTAACCGGTTAATATCCCGCTGGGAGTACGTTCCGA 374
 QY 881 AGGTTAAATCTCAATGAAATGACGGGGGGCCCGACAAAGGGGTGAGACATGTGTTAAT 940
 Db 373 AGAATGAATCTCAAGGAATGACGGGGGGCCCGACAAAGGGGTGAGACATGTGTTAAT 314
 QY 941 TCGAAGCAACGGGAGAACTTACTACTCTTTGACATCCACAGAACATTTGAGAGATCAG 1000
 Db 313 TCGATGCAAGGAGAACTTACTACAGGCTTGAACATCCCGCAATCTTTGAAAGAGA 254
 QY 1001 ATGTGCTCTTGGGAACTGTGAGACAGTGTCTCATGCTGTCTCACTCTGTGTTGA 1060
 Db 253 GGGGTGCTCTGGGAAACCGGACACAGGTGTGTGATGCTGTCTCACTCTGTGCGCTAA 194
 QY 1061 AATGTTGGTTAATGTCCTGTAACGAGCGCAACCTTGTCTTATTTGCCAGACGTAAAG 1120
 Db 193 GGTGTTGGTTAATGTCCTGTAACGAGCGCAACCTTGTCTTATTTGCCA--CCGTTGAG 136
 QY 1121 GTGGAACTTTAAGAGAGATGCGCGTGAACAACCGAGAGAAAGTGGGAGACAGCTCAAGT 1180
 Db 135 TTGGAACTTTAAGAGAGATGCGCGTGAACAACCGAGAGAAAGTGAAGATGAGCTCAAGT 76
 QY 1181 CATCATGCGCTTAAAGAGATGAGGCTGACACGTCTCATATGGCGCTATACAGAGGCTCG 1240
 Db 75 CATCATGCGCTTAAAGAGATGAGGCTGAGACACGTCTCATATGGCGGACAAAGGCTCG 16
 QY 1241 AAGCTAAGCATATAGT 1255
 Db 15 GATCCCGGAGGGTG 1

RESULT 5
 BH705272 1079 bp DNA linear GSS 20-FEB-2002
 LOCUS BOMKA47TF BO_2_3 KB Brassica oleracea genomic clone BOMKA47,
 DEFINITION genomic survey sequence.
 ACCESSION BH705272 GI:18787746
 VERSION BH705272.1 GI:18787746
 KEYWORDS
 SOURCE
 ORGANISM
 Brassica oleracea
 Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; euroside II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 1079)
 REFERENCE
 Town,C.D., Van Aken,S., Utebback,T., Koo,H. and Fraser,C.M.
 Whole genome shotgun sequencing of Brassica oleracea
 Unpublished
 OTHER DBS: BOMKA47TF
 CONTACT: Chris Town

TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TF
 Class: sheared ends.
 FEATURES
 source
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 /organism="Brassica oleracea"
 /mol_type="genomic DNA"
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 /db_xref="taxon:3712"
 /clone="BOMKA47"
 /clone_1="BO_2_3_KB"
 /note="vector: pHD51, Site_1: BstXI, 2-3 kb sheared
 genomic DNA inserted into pHD51 using BstXI linkers"
 BASE COUNT 265 a 257 c 353 g 204 t

ORIGIN
 Query Match 40.0%; Score 594; DB 28; Length 1079;
 Best Local Similarity 74.0%; Pred. No. 1,4e-164;
 Matches 805; Conservative 0; Mismatches 255; Indels 28; Gaps 3;

QY 174 GAAAGAGGGAGCTCTTGGAGCTTCCGCTATTAATAGACCTGGGTAGATTAAGTCTG 233
 Db 17 GTAGGCTGAAGAGCAATATAGAAATCCGCCAGAGAGGGCTCGGCTGTGATTAGCTAG 76
 QY 234 TTGTAGAGGTAAAGGCTTACCAAGGCAAGATCTTACTGTGCTGAGAGATGACAGT 293
 Db 77 TTGTAGAGCAATATGCTTACCAAGGCAAGATGATAGTGTGCTGAGAGATGATCAG 136
 QY 294 CACACTGGAGCTGAGACACGCGCAACTCTTAACGGAGGCAAGAGTGGGAAATATGGA 353
 Db 137 CACACTGGAGCTGAGACACGCGCAACTCTTAACGGAGGCAAGAGTGGGAAATATTCG 196
 QY 354 CAATGGGCGCAAGCTGATCCAGCCATGCGCGGTGTGTGAAGAAGGCTTAGGGTTGTA 413
 Db 197 CAATGGGCGCAAGCTGATCCAGCCATGCGCGGTGTGTGAAGAAGGCTTAGGGTTGTA 256
 QY 414 AGCACTTTCAGGGGTGAGAAAGGTGATAGATTATACGTTATCATCTTGAAGTACCC 473
 Db 257 ACTTCTTTCAGAGAGAAAG-----CAATGACGATATCTG 293
 QY 474 CAGAAAGAGACCGGCTTAATCTGTGTCAGACGCGCGGTAAATACAGAGGTCGAAGCT 533
 Db 294 GGGAAATAGCACTGGCTTAATCTGTGTCAGACGCGCGGTAAATACAGAGGTCGAAGCT 353
 QY 534 TAATCGAATTAATCTGGGCTTAAGCGGCGCTAGAGTGTGTTAATCGATGATGTAATC 593
 Db 354 TATCCGGAATGATTTGGCGTAAAGCGTGTAGTGTGCTTTTAATCCGCGCTGAATTC 413
 QY 594 CCAAGGCTCAACTTGGAAATGCAACCGATCTGCTAGTATGATGTGAGGGCTG 653
 Db 414 CCAGGCTCAACTTGGAAATGCAACCGATCTGCTAGTATGATGTGAGGGCTG 473
 QY 654 TGAATTTCTGCTAGCGGTGAATGCGTATATAGAAAGGACATAGTGGCAAG 713
 Db 474 GGAATTTCTGCTAGCGGTGAATGCGTATATAGAAAGGACATAGTGGCAAG 533
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 Db 594 ATACCTGATGATCCAGCGGTAAAGATGCTACTAGCGCTG---GGTGAATGACT 653
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 Db 654 CAGTGTGTAGCTAAGCGTTAATAGTATCCCGCTGGGAGTATGCTTCGCAAGATGAAC 713
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 QY 1011 CGGAACTGTGAGACAGGTGCTGATGCTGTGTAGCTCTGTGTGTGAATGTTGGGT 1070
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 QY 1071 TAACTCCGTTAACGAGGCAACCTTGTCTTTTTCAGAGCAGTAAATGTGTGAACTT 1130
 Db 894 TAACTCCGTTAACGAGGCAACCTTGTCTTTTTCAGAGCAGTAAATGTGTGAACTT 951
 QY 1131 TAAAGAACTGCGGTGACAAACCGAGAGAGGTGAGAGACAGCTCAAGTCAATGAGCC 1190
 Db 952 CTGACAGACTGCGGTGATAGCCGAGAGAGGTGAGAGTGAAGTCAAGTCAATGAGCC 1011

QY 1191 CTTACGAGTATGGGCTTACACAGCTGCTACATAGCGCTATACAGAGGGCTTGCAAGTACGCA 1250
 DB 1012 CTTATGGCTTGGGCGACACAGCTGCTATCATGCGCGGACAAAGGCTGCGATCCCGGCA 1071
 QY 1251 TAGTGAGC 1258
 DB 1072 GGGTGAGC 1079

RESULT 6
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 DEFINITION genomic survey sequence.
 ACCESSION BZ463550
 VERSION BZ463550.1 GI:26749465
 KEYWORDS GSS.
 SOURCE Brassica oleracea
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 / eustosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 1044)
 Town,C.D., Van Aken,S., Uteback,T., Koo,H. and Fraser,C.M.
 Whole genome shotgun sequencing of Brassica oleracea
 Unpublished
 Other_GSSs: BONK86TR
 COMMENT Contact: Chris Town

REFERENCE
 AUTHORS Town,C.D., Van Aken,S., Uteback,T., Koo,H. and Fraser,C.M.
 TITLE Whole genome shotgun sequencing of Brassica oleracea
 JOURNAL Unpublished
 COMMENT Other_GSSs: BONK86TR
 Contact: Chris Town

TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TP
 Class: sheared ends.

FEATURES
 source
 Location/Qualifiers
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 /organism="Brassica oleracea"
 /mol_type="genomic DNA"
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 /db_xref="taxon:3712"
 /clone="BONK86"
 /clone_1ib="BO.1.6.2_KB_tot"
 /note="Vector: pHOSt; Site 1. BatXI; 1.6-2 kb sheared
 total DNA inserted into pHOSt using BatXI linkers"
 BASE COUNT 199 a 327 c 261 g 257 t
 ORIGIN

Query Match 39.8%; Score 591.4; DB 29; Length 1044;
 Best Local Similarity 77.0%; Prid. No. 8.1e-164;
 Matches 760; Conservative 0; Mismatches 221; Indels 6; Gaps 3;
 QY 462 TGACGTAGCCCGGAGAGAGACACCGGCTAATCTGTGACAGAGCGCGGCTTGAATGTC 521
 DB 999 TGACGTAATCTGGGGAATAGCATCGGCTTACTCTGTGCAAGACCGCGGTAATACGA 940
 QY 522 GGGTGCAAGCGTTAATCGAATTAATCTGGGCGTAAAGCGCGCGTAAAGTCTTTGAATGTC 581
 DB 939 GGATGCAAGCGTTAATCGGGAATGATGGCGTAAAGCGTGTAGGTGCTTTTAAATGTC 880
 QY 582 GGATGTAATCCAGAGGCTCAACCTTGGAAATGGACCCCGATATCGGCTAGCTAAGTAT 641
 DB 879 CGCGCTCAATCCAGAGGCTCAACCTTGGAAATGGACCCCGATATCGGCTAGCTAAGTAT 820
 QY 642 GGTAGAGGGGTGTGAAATTTCTGTAGCGGTGAATATCGTATATAGAAAGGAACAT 701
 DB 819 GGTAGGGGACAGAGGAATTTCCGTTGAGGGGTGAATATCGTATAGATCGAAAGAACAC 760
 QY 702 CAGTGGGAAGCGACACCTGTGACATATCTGACACTAGGTCGAAAGCGTGGGAGC 761
 DB 759 CAACGGCGAAGACCTCTGCTGGGCGACACTGACACTAGAGAGCAAGGCTAAGGGAGC 700

QY 762 AACACGATATGATATCCCTGTAGTCCACGCGCTTAAAGATGTCTACTAGCCGTG--G 818
 DB 699 GAATGGATATGATATCCCAATAGTCTTACGCGCTTAAAGATGATCTAGGCGCTTGCG 640
 QY 819 GTTGTAAATGACTTATGCGGAGCTTACGCAATATAGTACCGGCTGGGAGTACGCGCG 878
 DB 639 TATGACCCCGTACATGCTGTAGCTAAGCTTAAAGTATCCCGCTGGGAGTACGTTCC 580
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 QY 939 ATTGGAAGAACGCAAGAACCTTACCTACTCTTGATATCCAGACGAACTTTGAGAGATC 998
 DB 519 ATTGATGCAAGCAAGAACCTTACCTACTCTTGATATCCAGACGAACTTTGAGAGATC 460
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 DB 459 GAGGGGTGCTTGGGAACTGTGACAGAGTGTGCAATGCTGTGCTGCTGCTGTTGT 400
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 QY 1119 TGGTGGAACTTTAAGAGACTCCGCTGACAAACCGAGAGAGTGGGAGCACTGCAA 1178
 DB 341 AGTTGGAACTTTAAGAGACTCCGCTGACAAACCGAGAGAGTGGGAGCACTGCAA 282
 QY 1179 GTTCATCATGCGCTTACAGATGAGGCTTACACAGTGTCTTACATGCGTATACAGAGGCT 1238
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 QY 1239 GCAAGCTAGCATGATGAGCGAATCCCAAGATACGTCGATGCGGATGAGTGC 1298
 DB 221 GCGATCCCGGAGGATGAGCTAATCCCAAGATACGTCGATGCGGATGAGTGC 162
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 QY 1358 AGTTCCCGGAGGCTTGTACACAGCGCGCTGACACGATGAGTGTGATGATGATGATGAT 1417
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RESULT 7
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 LOCUS BONHR54TR.B0.1.6.2_KB_for_Brassica_oleracea_genomic_clone_BONHR54,
 DEFINITION genomic survey sequence.
 ACCESSION BZ494182
 VERSION BZ494182.1 GI:27004681
 KEYWORDS GSS.
 SOURCE Brassica oleracea
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 / eustosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 1051)
 Town,C.D., Van Aken,S., Uteback,T., Koo,H. and Fraser,C.M.
 Whole genome shotgun sequencing of Brassica oleracea
 Unpublished
 Other_GSSs: BONHR54TR
 COMMENT Contact: Chris Town

TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208

Email: cdtown@ligr.org
DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TR
Class: sheared ends

FEATURES
Source Location/Qualifiers

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/mol_type="genomic DNA"
/strain="TO1000D3"
/db_xref="taxon:3712"
/clone="BON228"
/clone_lib="BO_1.6.2_KB_tot"
/note="Vector: pHOSt; Site 1: BstXI; 1.6-2 kb sheared
total DNA inserted into pHOSt using BstXI linkers"
BASE COUNT 202 a 332 c 259 g 258 t
ORIGIN

Query Match 39.8%; Score 591.4; DB 29; Length 1016;
Best Local Similarity 77.0%; Pred. No. 8.1e-164;
Matches 760; Conservative 0; Mismatches 221; Indels 6; Gaps 3;
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999 TGACGTTAGCCCCAGAGAGACACCGGCTAAGTCTGCGACAGACCGCGTAAATACAGA 940
522 GGGTGCAGACGTTAATCGGAATTACTGCGCGTAAAGCGCGGTAGTGTGTTTAAAGTC 581
999 GGGTGCAGACGTTAATCGGAATTACTGCGCGTAAAGCGCGGTAGTGTGTTTAAAGTC 880
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762 AAAGAGATTAGATACCTGATTAATCTGACACTGAGCGGAAACCGTGGGAGAC 818
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639 TATGACCCCGTGAAGTGTGCTAGCTTAACGCGTTAAGTATCCCGCTGGGAGATACCGCG 580
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281 GTCAATCATGCGCTTACAGAGTGGGCTACACAGGTGCTAATGAGGTATACAGAGGCT 222

1239 GCAAGTACGAGATAGTACGAGATCCACAAATACGTTAGTCCGATGAGATCTC 1298
221 CGGATCCCGGAGAGTACGATTAATCTCAAAACCCCTCTCACTTGGATTGAGGCTCC 162
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1358 ACGTTCGCGGCGCTTGTACACACCGCGCTACACCATGAGGAGTGTATGCTCCAGAGT 1417
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41 CGTACCTTAACCGCAAGAGAGGAGG 15

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LOCUS B2426201 1016 bp DNA linear GSS 13-DEC-2002
DEFINITION BOND228Tf BO_1.6.2_KB_tot Brassica oleracea genomic clone BOND228,
genomic survey sequence.
ACCESSION B2426201
VERSION B2426201.1 GI:26667713
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
1 (bases 1 to 1016)
TOWN, C.D., Van Aken, S., Uterback, T., Koo, H. and Fraser, C.M.
REFERENCE
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished
COMMENT Other GSSs: BOND228TR
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@ligr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.

FEATURES
Source Location/Qualifiers

1..1016
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000D3"
/db_xref="taxon:3712"
/clone="BOND228"
/clone_lib="BO_1.6.2_KB_tot"
/note="Vector: pHOSt; Site 1: BstXI; 1.6-2 kb sheared
total DNA inserted into pHOSt using BstXI linkers"
BASE COUNT 193 a 328 c 239 g 256 t
ORIGIN

Query Match 39.7%; Score 590.4; DB 29; Length 1016;
Best Local Similarity 76.0%; Pred. No. 1.6e-163;
Matches 792; Conservative 0; Mismatches 221; Indels 29; Gaps 4;
212 GAGCGTGGCGTGAATAGTATGTTGTTAGGTTAAAGGCTTACCAAGGCGAGCATCTTAA 271
1016 GGGGTGGCGTGTATTAAGTATGAGTGAAGGCAATAGCTTACCAAGGCGATGATGATG 957
272 CTGCTGAGAGATGACCAATCACTGGGACTGAGACAGCGCCCAAGCTCTTACGGGA 331
956 CTGCTGAGAGATGATGACCAATCACTGGGACTGAGACAGCGCCCAAGCTCTTACGGGA 897
332 GCGAGAGTGGGGAATATGCAATGAGCGCAAGCTGATCAGCCATGCGCGCTGTGT 391
896 GCGAGAGTGGGGAAT- TTCCGCAATGGCGCAAGACCTGATCAGCAATGCGCGCTGTGAG 838

QY 392 GAAGAAAGCCTTAGGTTGTAAGACCTTCAGGGGTGAGGAAGGTGATAGTTAATAC 451
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 QY 452 GTATATCTTTCAGGTTAGCCCGAGAGAGACCGGTTAACTCTGTGTCCAGACCGCG 511
 DB 793 -----CATGACGGTATCTGGGGATATAGCATGGGCTAATCTGTGTCCAGACCGCG 741
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 QY 632 GCTAAGATAGTGAAGGGGTGTGAATTTCTGTGTAGCGGTGAATGCGTATAGTATAG 691
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 QY 692 GAAGAAACATTCAGTGGCGAGAGGAGACACCTTGAATTTACTGTACACTGAGAGTGGAGAG 751
 DB 560 GAAGAAACATTCAGTGGCGAGAGGAGACTTGTGTGGCGAGACTGTACACTGAGAGAGAGAG 501
 QY 752 CGTGGGAGCAACAGAGATTAGTACCCTGTGTGTCAAGCGGTGAATGATGTCTATAG 811
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 QY 1049 CTGT 1108
 DB 200 CTGT 141
 QY 1109 CACAGCATATGT 1168
 DB 140 CA---CGT 83
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RESULT 9
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 LOCUS BOMJ286Tf BO_2.3 KB Brassica oleracea genomic clone BOMJ286.
 DEFINITION genomic survey sequence.
 ACCESSION BH656222
 VERSION BH656222.1 GI:18714532
 KEYWORDS GSS.
 SOURCE Brassica oleracea
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; rosids

REFERENCE : eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 1031)
 AUTHORS Town,C.D., Van Aken,S., Uterback,T., Koo,H. and Fraser,C.M.
 TITLE Whole genome shotgun sequencing of Brassica oleracea
 JOURNAL Unpublished
 COMMENT Contact: Chris Town
 TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TF
 Class: sheared ends.
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 /mol_type="genomic DNA"
 /strain="T01000D3"
 /db_xref="taxon:3712"
 /clone_jid="BO_2.3 KB"
 /note="Vector: pROSL; Site 1: BstXI; 2-3 kb sheared genomic DNA inserted into pROSL using BstXI linkers"
 BASE COUNT 198 a 327 c 250 g 256 t
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 Query Match 39.7% Score 589.8; DB 28; Length 1031;
 Best Local Similarity 74.9%; Pred. No. 2,46-163; Indels 28; Gaps 3;
 Matches 790; Conservative 0; Mismatches 237;
 QY 320 ACTCTTACGGAGAGCAGAGTGGGGAATTTGACAAATGGCGCGACCTGATCCAGCA 379
 DB 1031 ACTCTTACGGAGAGCAGAGTGGGGAATTTTCCCAATGGCGCAACCTCGAGAGCA 972
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 DB 971 TGGCGGTGTGTGAAGAGGCTTAGGGTTGTAAGACCTTCTTCCAGAGAGAGAG---- 916
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 DB 874 CAGAGAGCGGGTTAATCAGAGGTCGCAAGCCTTATCGGAATTAATGGGCGTTAAAGCG 815
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 DB 814 TCTGTAGGT 755
 QY 620 CGATCTGT 679
 DB 754 GGAACATCAAGCTTGT 695
 QY 680 GCGTATATAGAGAGAGAACATCAGTGGCGAGAGCGCACACCTTGAATTAATCTGACACT 739
 DB 694 GCGTATATAGAGAGAGAACATCAGTGGCGAGAGCGCACACCTTGAATTAATCTGACACT 635
 QY 740 GAGTGTGCAAGAGCTGTGGAGCAACAGATTAGATACCTGTGTGTGTGTGTGTGTGTGT 799
 DB 634 GAGAGAGCAAGAGCTGTGGAGCAACAGATTAGATACCTGTGTGTGTGTGTGTGTGTGT 575
 QY 800 GATGTCTACTAGCGGTG---GGTGTATATAGTGTGGGCGAGTAAAGCATATAGTA 856
 DB 574 GATGTCTACTAGCGGTG---GGTGTATATAGTGTGGGCGAGTAAAGCATATAGTA 515
 QY 857 GACCGCTGTGGAGTACGCGCGCAAGTTAAACTCAATGATTTGACGGGGGCGCGCAC 916
 DB 514 TCCCGCTGTGGAGTACGCGCGCAAGTTAAACTCAATGATTTGACGGGGGCGCGCAC 455
 QY 917 AAGCGTGTAGAGATGTGTTAATTCGAAGACCGAGAACTTACTACTTGTACA 976

Db 454 AAGCGGTGAGCATGTGTTTAAATTCGATGCAAGGAGAACTTACAGGGCTTGACA 395
 QY 977 TCACAGACATTGTAAGATCAAGATGTGCTTCCGAACTGTGACAGAGTGTGCAT 1036
 Db 394 TGCCGCAATCCTTTAAAGAGAGGGGTGCTTCCGAAACCGGACACAGGTGTGCAT 335
 QY 1037 GGCTGTGTGAGCTCGTGTGTGAAATGTGGGTAAAGTCCGTAAAGAGGCAACCTT 1096
 Db 334 GGCTGTGTGAGCTCGTGTGTGAAATGTGGGTAAAGTCCGTAAAGAGGCAACCTT 275
 QY 1097 GTCTTATTTGCGACACGTAAATGTGGGAACTTTAAGAGACTGCGGTGACAAACCGG 1156
 Db 274 GTGTTAGTTGCCA--CCGTTGAGTTGAAACCTTGAACAGACTGCGGTGATAAGCCGG 217
 QY 1157 AGAAGGTGGGAGAGAGTCAAGTCAATGATGAGGCTTAAAGAGAGTGAAGAGTCTT 1216
 Db 216 AGAAGGTGGGAGAGTCAAGTCAATGATGAGGCTTAAAGAGAGTGAAGAGTCTT 157
 QY 1217 ACAATGGCTATACAGAGGCTGCAAGCTAGCATAGAGGCAATCCACAAAGTACGT 1276
 Db 156 ACAATGGCTGAGAAAGGTGCGATCCCGGAGGTGAGCTTAACTCCAAAACCGCTC 97
 QY 1277 CGTGTGCGGATTTGAGCTGTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1336
 Db 96 CTGATGCGGATTTGAGCTGCAAGCTGCAAGCTGCTGCTGCTGCTGCTGCTGCTG 37
 QY 1337 AATCAGATGTCAAGGCTGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1371
 Db 36 GGTGAGCCATACGGCGGAAATTCGTCGCGGCT 2

RESULT 10
 CD042372 741 bp mRNA linear EST 09-MAY-2003
 LOCUS CD042372.1 GI:30495965
 DEFINITION psHB040x24f_302263 psHB: Infected hypocotyl soybean host. 48 hrs post infection. Phytophthora sojae cDNA clone SHB040F24 5, mRNA sequence.

ACCESSION CD042372
 VERSION CD042372.1
 KEYWORDS EST,
 SOURCE Phytophthora sojae
 ORGANISM Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae; Phytophthora.

REFERENCE 1 (bases 1 to 741)
 AUTHORS Tyler, B.M., Juelson, H.S., Giljen, M., Dean, R.A. and Waugh, M.E.
 TITLE USDA-IPAFs: Expression of Phytophthora sojae genes during infection and propagation

JOURNAL Unpublished
 COMMENT Contact: Tyler B
 Tyler Lab

ABI
 1880 Pratt Dr., Blacksburg, VA 24061, USA
 Tel: 540-231-7318
 Email: bmtyle@vt.edu
 PCR Primers
 FORWARD: BK reverse
 Plate: 040 row: F column: 24
 Seq primer: BK reverse
 High quality sequence stop: 741.
 Location/Qualifiers

FEATURES

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 /mol_type="RNA"
 /db_xref="taxon:67593"
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 /issue_type="infected host tissue"
 /cell_line="P6497"
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 /clone_id="psHB: Infected hypocotyl soybean host. 48 hrs post infection"
 /note="Vector: PBK-CMV, Site_1: EcoRI, Site_2: XhoI; USDA-IPAFs: Expression of Phytophthora sojae genes during

BASE COUNT 159 a 230 c 164 g 187 t 1 others
 ORIGIN

Query Match 39.6%; Score 588.6; DB 14; Length 741;
 Best Local Similarity 88.8%; Pred. No. 4,5e-163;
 Matches 659; Conservative 0; Mismatches 80; Indels 3; Gaps 2;

QY 366 GCTGATCCAGCCATGCGCGGTGTGTGAAAGAGGCTTAAAGGATCTTACG 425
 Db 741 GCTGATCCAGCCATGCGCGGTGTGTGAAAGAGGCTTAAAGGATCTTAA 682
 QY 426 GTGAGAGAGGATAGATTATAGTATCATCTTACGTTAGCCCAAGAGGAC 485
 Db 681 GG-GAGAGAGGCTTAAAGGATAGTATCATCTTACGTTAGCCCAAGAGGAC 623
 QY 486 CGGCTACTGTGTCCAGAGCGCGGTATACAGAGGCTGCAAGCTTAAATCGAATTA 545
 Db 622 CGGCTAACTGTGTCCAGAGCGCGGTATACAGAGGCTGCAAGCTTAAATCGAATTA 563
 QY 546 CTGGGGGTAAAGCGCGGTAGGTGTTTAAAGTGGATGAAATCCAGGGCTCAAC 605
 Db 562 CTGGGGGTAAAGCGCGGTAGGTGTTTAAAGTGGATGAAATCCAGGGCTCAAC 503
 QY 606 CTGGAGATGCAACCGGATACCTGCTAGCTAGAGTGTGTAAGGGGTGAAATTTCTG 665
 Db 502 CTGGAGATGCAATCCAAATCTGTGTGCTAGAGTGTGTAAGGGGTGAAATTTCTG 443
 QY 666 TGTAGGTGTAAGTGTGATATAGAGAACTATGTCGGAAGGCGACACCTTGA 725
 Db 442 TGTAGGTGTAAGTGTGATATAGAGAACTATGTCGGAAGGCGACACCTTGA 383
 QY 726 CTATATGACACCTGAGTGTGCAAGCGTGGGAGCAACAGATTAATATCCTGTAG 785
 Db 382 CTATATGACACCTGAGTGTGCAAGCGTGGGAGCAACAGATTAATATCCTGTAG 323
 QY 786 TCCAGCCGTTAAACGATGTTACTAGCCGTGGTT--GTATGACTTAGTGGCGACGT 843
 Db 322 TCCAGCCGTTAAACGATGTTACTAGCCGTGGTT--GTATGACTTAGTGGCGACGT 263
 QY 844 AACGCAATAGTAGACCGCGTGGGAGTACGGCGCAAGTTAAATCAATGAATGA 903
 Db 262 AACGCAATAGTAGACCGCGTGGGAGTACGGCGCAAGTTAAATCAATGAATGA 203
 QY 904 CGGGGGCCGCAACAGCGGTGAGCATGTGTTTAAATGAGCAACCGGAACCTTA 963
 Db 202 CGGGGGCCGCAACAGCGGTGAGCATGTGTTTAAATGAGCAACCGGAACCTTA 143
 QY 964 CCTACTCTGACATCCAGACATTTAGAGATGAGATGAGTGGCTTGGGAACGTGAG 1023
 Db 142 CCTACTCTGACATCCAGACATTTAGAGATGAGATGAGTGGCTTGGGAACGTGAG 83
 QY 1024 ACAAGTGTGCAATGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1083
 Db 82 ACAAGTGTGCAATGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 23
 QY 1084 GAGCGCAACCTTGTCTTATT 1105
 Db 22 GAGCGCAACCTTGTCTTATT 1

RESULT 11
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 LOCUS B2450751
 DEFINITION BOMB63TR BO_1.6_2_KB_tot Brassica oleracea genomic clone BOMB63,
 genomic survey sequence.
 ACCESSION B2450751
 VERSION B2450751.1
 KEYWORDS GSS,
 SOURCE Brassica oleracea
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids

REFERENCE : eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 1077)
AUTHORS : Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
TITLE : Whole genome shotgun sequencing of Brassica oleracea
JOURNAL : Unpublished
COMMENT : Other GSSs: BONB063TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdlowne@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
Source
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/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO100DH3"
/db_xref="taxon:3712"
/clone="BONB063"
/clone_lib="BO_1.6_2_KB_tot"
/note="Vector: pHOSt1; Site 1: BstXI; 1.6-2 kb sheared
total DNA inserted into pHOSt1 using BstXI linkers"

BASE COUNT 263 a 267 c 342 g 205 t
ORIGIN

Query Match 39.6%; Score 587.8; DB 29; Length 1077;
Best Local Similarity 76.9%; Pred. No. 9.6e-163;
Matches 757; Conservative 0; Mismatches 222; Indels 6; Gaps 3;

QY 462 TCACGTAGCCCGAGAAAGACCGGGCTTACTGTGTCACAGCCCGGTAAATACAGA 521
DB 69 TACCGTATCTGGGGAATAGCATCGGCTACTCTGTGTCACAGCCCGGTAAATACAGA 128
QY 522 GSGTGCAGCGTTAATCGGAATTAATCTGSGCGTAAAGCCGCGTGTGTTAAGTC 581
DB 129 GGAATGCAAGGTTATCCGGAATGATGGCGTAAAGCGTCTGTAGTGGCTTTTAAGTC 188
QY 582 GGAATGCAATCCCAAGGCTCAACCTTGGAATGGACCGGATCTAGCTAGAGTAT 641
DB 189 CGCCCTCAATCCCAAGGCTCAACCTTGGAATGGACCGGATCTAGCTAGAGTAT 248
QY 642 GGTAGAGGGGTGTGAATTTCTGTGTAGCCGTGAATTCGTATATAGAGAGAAAT 701
DB 249 GGTAGAGGGGTGTGAATTTCTGTGTAGCCGTGAATTCGTATATAGAGAGAAAT 308
QY 702 CAGTGGCGAAGGAGACCTCTGATCTAATCTGATGACATGAGTGGAGAGCGTGGAGC 761
DB 309 CACCGGCGAAGGAGACCTCTGATCTAATCTGATGACATGAGTGGAGAGCGTGGAGC 368
QY 762 AACAGGATTAGTACCTCTGATCTAATCTGATGACATGAGTGGAGAGCGTGGAGC 818
DB 369 GAATGGATTAGTACCTCTGATCTAATCTGATGACATGAGTGGAGAGCGTGGAGC 428
QY 819 GTTGTATAGTCTAGTGGCGCAGCTTAACTAATAGTAAACCGCTGGGGAGTACGGCG 878
DB 429 TATCGACCCGTGACGCTGTACTAATCCGTTAATGATCCCGCTGGGGAGTACGGCG 488
QY 879 CAAGGTTAAATCAATGATGATGACGGGGGCGCGACAGCGGTGAGAGATGGTTA 938
DB 489 CAGGAATGAATCAATGATGATGACGGGGGCGCGACAGCGGTGAGAGATGGTTA 548
QY 939 ATTGGAAGCAACCGGAACCTTACTTACTTGAATCCAGAGACATTTAGAGATC 998
DB 549 ATTGGAAGCAACCGGAACCTTACTTACTTGAATCCAGAGACATTTAGAGATC 608
QY 999 AGATGATGCTTGGGGAATGTGAGACAGGTGATGATGATGATGATGATGATGATGAT 1058
DB 609 GAGGGTGTCTTGGGGAATGTGAGACAGGTGATGATGATGATGATGATGATGATGAT 668
QY 1059 GAAATGTTGGGTTAAGTCCCGTAAGAGGCGCAACCTTGTCTTATTTGCGACAGCTAA 1118

DB 669 AAGGTGTTGGTTAAGTCCCGTAAGAGGCGCAACCTTGTCTTATTTGCGACAGCTAA 726
QY 1119 TGTGGAACCTTAAAGGAGACTGCGGCTGACCAACCGGAGAGGTGGGACAGCTCAA 1178
DB 727 AGTTGGAACCTTAAAGGAGACTGCGGCTGACCAACCGGAGAGGTGGGACAGCTCAA 786
QY 1179 GTCATATGCGCCTTACGAGTGGGCTACACAGTGTCTAATAGGCGGTATACAGAGGCT 1238
DB 787 GTCATATGCGCCTTACGAGTGGGCTACACAGTGTCTAATAGGCGGTATACAGAGGCT 846
QY 1239 GCAAGCTAGCGATAGTGGAGCAATCCCAAAAGTACGTCTAGTCCGATTTGAGCTCG 1298
DB 847 GCGATCCCGGACAGGTAGTACTCAAAACCGGCTCTAGTGGATGAGAGCTCG 906
QY 1299 AACTGACTCCATAGTGGAGTCTGATGATGATGATGATGATGATGATGATGAT 1357
DB 907 AACTGACTCCATAGTGGAGTCTGATGATGATGATGATGATGATGATGATGAT 966
QY 1358 AGCTTCCCGGCGCTTGTACACACCGCGTCAACACATGGAGTGTATGCTCCAGAGT 1417
DB 967 TCGTTCCTCCGCGCTTGTACACACCGCGTCAACACATGGAGTGTATGCTCCAGAGT 1026
QY 1418 AGCTTCCCTTAAACCTTCCGCGGATG 1442
DB 1027 TCGTACCTTAAACCTTCCGCGGATG 1051

RESULT 12
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LOCUS PUBRT547D.ZM.0.6.1.0.KB.Zea.mays.genomic.clone.ZM87A032112,
DEFINITION genomic survey sequence.
ACCESSION B2685785
VERSION B2685785.1 GI:28245311
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 899)
AUTHORS Whitehead, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick
A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Benneken, J.
TITLE Maize Genomics Consortium
JOURNAL Unpublished
COMMENT Contact: Cathy Whitehead
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitehead@tigr.org
Seq primer: TP
Class: sheared ends.

FEATURES
Source
1..899
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZM87A032112"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"

BASE COUNT 182 a 293 c 211 g 213 t
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Query Match 38.8%; Score 576; DB 29; Length 899;
Best Local Similarity 80.0%; Pred. No. 2.7e-159;
Matches 728; Conservative 0; Mismatches 155; Indels 29; Gaps 4;
QY 331 AGGACGACGTGGGGAATTTGACATAGGGCGCAAGCTTATCCAGCGATCGCGGTGTG 390

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Db      899 AGGACGACGTGGGGAATTTGGACATGGGGCGCAGCCTGATCCAGCATGCCCCGTGAG 840
Qy      391 TGAAGAGGCGCTTAGGGTTGTAAGACATTTCAAGGGGTGAGAGGGTGAATAGTTAATA 450
Db      839 TGAATAGGCGCTTAGGGTTGTAAGACATTTCAAGGGGTGAGAGGGTGAATAGTTAATA 450
Qy      451 CGTTATCATCTTTGACGTTTACGCCCAAGAAAGACCGGCTTAACCTCTGTGTCCAGACCGCC 510
Db      804 CGGACGATTAATGACGCTGACCGGAAAGATTAAGCCCGGCTTAACCTCTGTGTCCAGACCGCC 745
Qy      511 GGTATATACAGAGGGGCGCAAGCGTTAATCCGAAATTAATCTAGGGCGTAAAGCGGGTAGTGG 570
Db      744 GGTATATACAGAGGGGCGCTAAGCGTTGCTCTGGAATCACTGGCGTAAAGCGGGTAGTGG 685
Qy      571 TTTGTTAAGTCGATGTGAAATCCAGGGCTCAACCTTGGAATGGAACCGGATACGGCT 630
Db      684 CCATTCAGTCGGGGGTGAAGCCTGTGGCTCAACACAGAAATGTCCTTGATACGTTT 625
Qy      631 AGCTAGATATAGTAGAGGGGTGTGGAATTTCTGTGTACCGGTGAATTCCTAGATATA 690
Db      624 GGTGATGATTTGTAGAGGTGTGTGGAATCTGCGAGGTGAGAGGTGAATTCCTAGATATA 690
Qy      691 GGAAGAAATCATCAGTGGCGAAGCGGACACCTTGACTAATATGACACTGAGGTGGGAA 750
Db      564 CGAAGAAACACCAAGTGGCGAAGCGGCGCAACTGAGCAACACTGACGCTGAGGCGGAA 505
Qy      751 GCGTGGGAGCAAAACAGATTAGATACCTGTGTGTGTCACCGCGTAAACGATGTCTACTA 810
Db      504 GCGTGGGAGCAAAACAGATTAGATACCTGTGTGTGTCACCGCGTAAACGATGTCTACTA 810
Qy      811 GCCGTTGGGTTG-TAATGACTTAGTGGCGGAGCTTAACGCAATTAAGTAGACCGGCTGGGA 869
Db      444 GCTGTGGGGGTGCTTGACCTCAGTAGCGAGCTTAACGCTTTAAGCATTCGCGCTGGGA 385
Qy      870 GTACGCGCGCAAGGTTAAACTCAATGAATTAAGCGGGGCGCGCAACAGCGGTGAGCA 929
Db      384 GTACGCGCGCAAGGTTAAACTCAATGAATTAAGCGGGGCGCGCAACAGCGGTGAGCA 325
Qy      930 TGTGTTAATTTCAAGAGACGCGAAGACCTTAACCTAATCTTGACATCCACAGAACAT 989
Db      324 TGTGTTAATTTCAAGAGACGCGAAGACCTTAACCTAATCTTGACATCCGTCGTCATCC 265
Qy      990 TGAAGATCAGATGATGCTTCCGGAACCTGTGAGACAGTGTGACAGTGTGTGTGTCAGC 1049
Db      264 GGAAGATCAGATGATGCTTCCGGAACCTGTGAGACAGTGTGTCAGTGTGTGTGTCAGC 205
Qy      1050 TCGTGTGTGAAATGTTGGGTTAAGTCCCTTACAGAGCGCAACCTTGTGTCTTATTTGCC 1109
Db      204 TCGTGTGTGAAATGTTGGGTTAAGTCCCTTACAGAGCGCAACCTTGTGTCTTATTTGCC 145
Qy      1110 AGCAGTATGATGATGGAATTTAAGAGACTGCGCGGTGACAAACCG-GAGAGAGGTGGG 1168
Db      144 ATCA--TTCAATGTGGCACTCTAGAGAGCTGCCGGGTGATTAACCGCGAGAGAGGTGG 87
Qy      1169 ACGAGTCAAGTCAATCATGCGCTTACAGAGTGAAGGCTTACACAGTGTGTACATGGGTAT 1228
Db      86 ATGAGTCAAGTCAATCATGCGCTTACAGAGTGAAGGCTTACACAGTGTGTACATGGGTAT 27
Qy      1229 ACAGAGGCGTGAAGCTAGCGA 1250
Db      26 ACAGTGGGACCGGAAACCGCGA 5

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RESULT 13
BH647750      1054 bp   DNA      linear   GSS 19-FEB-2002
LOCUS      BH647750/c
DEFINITION  BOMND31TR BO.2.3 KB Brassica oleracea genomic clone BOMND31,
ACCESSION  BH647750
VERSION     BH647750.1 GI:18705298
KEYWORDS    GSS.
SOURCE      Brassica oleracea
ORGANISM    Brassica oleracea

```

```

REFERENCE
AUTHORS     Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE       Whole genome shotgun sequencing of Brassica oleracea
JOURNAL     Unpublished
COMMENT     Contact: Chris Town
TIGR        9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
FEATURES
SOURCE
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/clone_1b="BO.2.3 KB"
/notes="vector: pHOSt; Site 1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOSt using BstXI linkers"
BASE COUNT  201 a 334 c 263 g 256 t
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Query Match 38.5%; Score 571.6; DB 28; Length 1054;
Best Local Similarity 76.7%; Pred. No. 6e-158;
Matches 765; Conservative 0; Mismatches 224; Indels 9; Gaps 5;
Qy      480 AAGCAGCGCTTAATCTGTGTCAGCAGCGCGGTAAATACAGAGGTGCAAGCTTAATCG 539
Db      1054 AAGCAGCGCTTAATCTGTGTCAGCAGCGCGGTAAATACAGAGGTGCAAGCTTAATCG 995
Qy      540 GAATTAATGAGGCGAAGAGCGCGGTAGTGTGTTAAGTGAATGCAATTCACAG 599
Db      994 GAATTAATGAGGCGAAGAGCGCGGTAGTGTGTTAAGTGAATGCAATTCACAG 936
Qy      600 CTCACCTTGAATGACACCCGATGCTGCTAGTGAATGATAGTGAAGGGTGTGANT 659
Db      935 CTCACCTTGAATGACACCCGATGCTGCTAGTGAATGATAGTGAAGGGTGTGANT 876
Qy      660 TTCCGTGTGACCGGTGAATGCGTATATAGAGAGAACATCAGTGGGAGAGCGACAC 719
Db      875 TTCCGTGTGACCGGTGAATGCGTATATAGAGAGAACATCAGTGGGAGAGCGACAC 816
Qy      720 CTTGACTAATTAATGACACTGAGTGCAGAAAGCGTGGGAGCAACAGGATTAGTACC 779
Db      815 CTTGACTAATTAATGACACTGAGTGCAGAAAGCGTGGGAGCAACAGGATTAGTACC 756
Qy      780 TGTGATGACAGCGCGTGAAGATGTCTATGACCGTTG--GGTGTATGACTTAAGTG 836
Db      755 CAGTAGTCTAGCGCGTGAAGATGTCTATGACCGTTG--GGTGTATGACTTAAGTG 696
Qy      837 CGCAGCTAAGCAATAGTAGACCGCTGAGGAGTAGCGCGCAAGTTAAATCAAT 896
Db      695 TGTAGCTAAGCAATAGTAGACCGCTGAGGAGTAGCGCGCAAGTTAAATCAAT 636
Qy      897 GAATTAAGCGGGGCGGACACAGCGGTGAGCAATGTGTTAATTTGAAGCAACGGAAG 956
Db      635 GAATTAAGCGGGGCGGACACAGCGGTGAGCAATGTGTTAATTTGAAGCAACGGAAG 576
Qy      957 AACCTACTACTCTTGAACATCCAGAAACATTTGAGAGATCAGATGTGCTTGGGGA 1016
Db      575 AACCTACTACTCTTGAACATCCAGAAACATTTGAGAGATCAGATGTGCTTGGGGA 516
Qy      1017 CTGTGAGACAGGTGCTGATGCTGTGTCAGCTGTGTTGTTGAATGTTGGTTAAGTC 1076
Db      515 CGCGACACAGGTGCTGATGCTGTGTCAGCTGTGTTGTTGAATGTTGGTTAAGTC 456

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QY 1077 CCGTAACGAGCGGACCCCTTGTCTTATTTGCCAGACGTAATGTGGAACTTTAAGA 1136
 DB 455 CCGCAACGAGCGGACCCCTGTTAGTTGCCA--CCGTTAGTTTGAACCTGAAACA 398
 QY 1137 GACTGCCGTGACAAACCCGAGAGAGTGGGAGACGTCAGTCAATCATATGAGCCCTTACG 1196
 DB 397 GACTGCCGTGACAAACCCGAGAGAGTGGGAGACGTCAGTCAATCATATGAGCCCTTACG 338
 QY 1197 AGTAGGCTACACAGCTGCTACATGCGCTATACAGAGGCTGCAAGCTAGCAGTAGTGA 1256
 DB 337 CCCTGGGCGACACACCGTGTACATATGCGCGGACAAAGGCTGCGATCCCGAGAGGTGA 278
 QY 1257 GCGAATCCCAAAAGTACGTCGTAATGTCGGGATTTGAGTGTGCAATTGCACTTCATGAAGT 1316
 DB 277 GCTAATCTCAAAAACCCGTCCTGAGTTGCGATTGCAAGCTGCAACTGCTGCAATGAAGC 218
 QY 1317 CCGAATCGCTAGTAATCGTGAATCAG-AATGTCAACGTAATACCTTCCGGGCTTGTGA 1375
 DB 217 CCGAATCGCTAGTAATCGCGGTCAACCATACGGGCGTGAATGCTTCCGGGCTTGTGA 158
 QY 1376 CACACCGCCCGTACACACCATGGAAGTTATGTGTCAGAGTAGCTAGCTTAACCTTCG 1435
 DB 157 CACACCGCCCGTACACACTATGAGGAGCTGGCCATGCGCCGAAGTCGTTACTTAACC--GCA 100
 QY 1436 GGATGGCGGTTACCAAGAGTGTCAATGACTGGGT 1473
 DB 99 AGAGGGGGGTGCCGAGGAGGAGGCTAGTACTGAGT 62

RESULT 14
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 LOCUS BONKTS1TR.B0.1.6_2_KB_for_Brassica_oleracea_genomic_clone_BONKTS1,
 DEFINITION genomic survey sequence.
 BZ440868
 VERSION BZ440868.1 GI:26598161
 KEYWORDS GSS.
 SOURCE Brassica oleracea
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 1; eusteroideae; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 974)
 REFERENCE Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
 Whole genome shotgun sequencing of Brassica oleracea
 Unpublished
 JOURNAL Other GSSs: BONKTS1TF
 COMMENT Contact: Chris Town
 TIGR 712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TR
 Class: sheared ends.

FEATURES
 Location/Qualifiers
 1..974

Source
 /organism="Brassica oleracea"
 /mol_type="genomic DNA"
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 /clone="BONKTS1"
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 /note="Vector: pHOSt1; Site_1: BstXI; 1.6-2 kb sheared
 total DNA inserted into pHOSt1 using BstXI linkers"
 BASE COUNT 245 a 227 c 314 g 188 t
 ORIGIN

Query Match 38.1%; Score 566.2; DB 29; Length 974;
 Best Local Similarity 76.4%; Pred. No. 2.3e-156;
 Matches 746; Conservative 0; Mismatches 203; Indels 28; Gaps 3;

QY 250 CTACCAAGCGACGATCTCTTAATGTTGTGAGAGATGACCACTGGAATGAGA 309
 DB 17 CTTACAGGCGCATGATCAGTACTGTTCCGAGAGAAATGATCAGACACTGGGACTGAGA 76
 QY 310 CAGGCCCAAGATCTCTTAAGGAGAGGAGAGAGTGGGAAATTATGCAATATGGGCGCAAGCT 369
 DB 77 CAGGCCCAAGATCTCTTAAGGAGAGGAGAGAGTGGGAAATTTCCCAATATGGGCGCAAGCT 136
 QY 370 GATCCAGCATGCGCGGTGTGTGAAGAAAGCCTTAAGGTGTGAAGCACTTTCAGGGGTG 429
 DB 137 GACGAGCAATGCGCGGTGTGAAGAAAGCCTTAAGGTGTGAAGCACTTTCAGGGGTG 156
 QY 430 AGGAAGGAGTATAGTTTATACATCTTACATCTTACATCTTACATCTTACATCTTACATCTT 489
 DB 197 AAGAA-----CATAACGATATCTGGGAAATAGCATGAGC 253
 QY 490 TAATCTGTGCGAGCAGCGCGGTATATACAGAGGCTCAAGCCTTAATCGAAATTACTGG 549
 DB 234 TAATCTGTGCGAGCAGCGCGGTATATACAGAGGCTCAAGCCTTAATCGAAATTACTGG 293
 QY 550 GCGTAAAGGCGCGGTATGTTGTGTATGTCGATGTGAATTCGCGGCTCAACCTTG 609
 DB 294 GCGTAAAGGCTGTAGGTGCTTTTAAGTCCCGCTCAATTCGCGGCTCAACCTTG 353
 QY 610 GATGAGCAACCGATCTGCTAGCTAGATAGTATGATAGGAGGTGTGAATTTCTGTGA 669
 DB 354 GACAGGCGGTGAATCTACAAAGCTTATGATAGGATAGGAGGTGTGAATTTCTGTGA 413
 QY 670 GCGGTGAATGCGTATATATGAAAGAACTTCGTGCGAGCGCAACCTTGTGACTTA 729
 DB 414 GCGGTGAATGCGTATATGAAAGAACTTCGTGCGAGCGCAACCTTGTGACTTA 473
 QY 730 TACTGACATGAGTGTGCGAAAGCGTGGGAGCAACAGATATGATACCTGTGATGCA 789
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genomic survey sequence.

ACCESSION BZ474941
 VERSION BZ474941.1 GI:26776372
 KEYWORDS GSS.
 SOURCE Brassica oleracea
 ORGANISM Brassica oleracea
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosid II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 1069)
 Town, C.D., Van Aken, S., Uterback, T., Koo, H. and Fraser, C.M.
 TITLE Whole genome shotgun sequencing of Brassica oleracea
 JOURNAL Unpublished
 COMMENT Other GSSs: BONKR59TF
 Contact: Chris Town
 TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TR
 Class: sheared ends

FEATURES
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 /db_xref="taxon:3712"
 /clone="BONKR59"
 /clone_id="BO_1.6.2_KB_tot"
 /note="Vector: pHO51; Site: 1; BstXI; 1.6-2 kb sheared
 total DNA inserted into pHO51 using BstXI linkers"
 BASE COUNT 200 a 351 c 248 g 270 t
 ORIGIN

Query Match 37.5%; Score 557.2; DB 29; Length 1069;
 Best Local Similarity 73.3%; Pred. No. 1,1e-153;
 Matches 805; Conservative 0; Mismatches 238; Indels 55; Gaps 5;

QY 3 TAGCTCAGATTGAACGCTGCGGCGAGGCTTAAACATGCAATGCGATACCGCCCTGAGGGGAAAGAGG 62
 DB 1046 TGGCTCAGAGATGAGCGCTGCGGCGATGCTTACAC-CATGCAAGTCGGAGCGGAAGGCG 988
 QY 63 AGCTTGCTCTGCTGACGAGCGCGAGCGGCTGAGTACCGGTAGGATTTGCTTATG 122
 DB 987 -----TTTCCAGTCCGCGAGCGGCTGAGTAAACGCTTACCTGCTTGGG 941
 QY 123 AGGGGAGCAATGAGGAAAGCAATGCTAATACCGATACCGCCCTGAGGGGAAAGAGG 182
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 QY 243 TAAAGGCTTACCAAGGCGCAATCTTAATCTGCTGAGAGAGTGAACCACTCACTGGG 302
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 DB 558 TGAATGGGCTTAAAGCGGTAGTGTGTTTGTAAATGCGATGGAATCCAGAGCTC 499
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 QY 1080 TAAAGAGCGCAACCTTG 1097
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Search completed: January 30, 2004, 23:43:13
 Job time : 3503.17 secs

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 Db 716 TGACATGAGTGGCAAGCCGTGGGAGCAAAACAGATTAGATACCTGCTGACGCG 775
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 Db 776 CGTAAACGATGCTACTAGCCGTTGGAGCCCTTATGAGGCGAGCTTAACGCA 835
 QY 851 TAAATGACCCGCTGGGAGTAAGCCGCGAAGTTAAACTCAATGATTTGACGGGGC 910
 Db 836 TAAATGACCCGCTGGGAGTAAGCCGCGAAGTTAAACTCAATGATTTGACGGGGC 895
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 US-09-821-016-5
 ; Sequence 5, Application US/09821016
 ; Patent No. 648591
 ; GENERAL INFORMATION:
 ; APPLICANT: CANON INC.
 ; TITLE OF INVENTION: Polyhydroxyalkanoate Synthase and Gene Encoding the Same Enzyme
 ; FILE REFERENCE: 4051021
 ; CURRENT APPLICATION NUMBER: US/09/821,016
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: Microsoft Word
 ; SEQ ID NO: 5
 ; LENGTH: 1501
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas jessenii P161 ; Bp-7376
 ; FEATURE:
 ; US-09-821-016-5

Query Match 76.1%; Score 1131; DB 4; Length 1501;
 Best Local Similarity 88.2%; Pred. No. 0;
 Matches 1299; Conservative 0; Mismatches 165; Indels 9; Gaps 6;

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; Sequence 1, Application US/09745476
; Patent No. 6521429
; GENERAL INFORMATION:
; APPLICANT: CANON INC.
; TITLE OF INVENTION: Preparation of Poly-hydroxyalkanoic Acid
; FILE REFERENCE: 4351008
; CURRENT APPLICATION NUMBER: US/09/745,476
; CURRENT FILING DATE: 2000-12-26
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Microsoft Word
; SEQ ID NO 1
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jesseni; P161 ; FERM P-17445
US-09-745-476-1

Query Match 76.1%; Score 1131; DB 4; Length 1501;
Best Local Similarity 88.2%; Pred. No. 0;
Matches 1299; Conservative 0; Mismatches 165; Indels 9; Gaps 6;

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QY	1211	CGTGCTACAAATGGCGTTATACAGAGGGCTGCAGAGTGCAGTAAGTGAAGCAATCCCAAAA	1270
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US-09-748-205-1
; Sequence 1, Application US/09748205
; Patent No. 6586562
; GENERAL INFORMATION:

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: APPLICANT: Caron Inc.
: TITLE OF INVENTION: Polyhydroxyalkanoate, its manufacturing method, and microorganisms
: TITLE OF INVENTION: those are used for the method.

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; CURRENT APPLICATION NUMBER: US/09/748,205
; CURRENT FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 1

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; SEQ ID NO 1
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; LENGTH: 1501
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; TYPE: DNA
; ORGANISM: Pseudomonas jessenii 161 strain
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US-09-748-205-1

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Query Match	76.1%	Score 1131	DB 4	Length 1501
Best Local Similarity	88.2%	Pred. No. 0		
Matches 1239; Conservative	0	Mismatches 165	Indels 9	Gaps 6

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QY	73	TGCTGACGAGCGGCGGACCGGTGAGTAAACGGTGAAGAAATGCTGCTGTGAGGCGGACAA	132
Db	59	TGAAATTC- AGCGGCGGACCGGTGAGTAAATGCTTGGAATCTGCTGTGTATGGGGACAA	117
QY	133	CATGTGAAAACGATGCTAATACCGGCATACGCGCTGAGGGCGAAAAGAGGGGACCTTCG	192
Db	118	CGCTCTGAAAAGGAGACGCTAATACCCGCATACGCTCTTACGGGAGAAAGAGAGGGG- - CCTTC	175
QY	193	GAGCCTTCGCGCTTATGATGAGACGCTGCTGAGATTAGCTAGTTGATGAGTAAAGCCTTA	252
Db	176	GAGCCTTGCGCTATGAGATGAGCTAGGTCAGGATTAAGCTAGTTGATGAGTATAGGCTCA	235
QY	253	CCAAAGGACGACATCTCTTAATGCTGTGAGAGAGTAACAATTCACACTGGGACCTGAGAACAC	312
Db	236	CCAAAGGACGATCGCTAATCTGTCTGAGAGAGTAATAGTCACTGGAACTGMAACAC	295
QY	313	GAGCCACGACTCTTACGGGAGCAGCAGTGGGAAATATTGACATATGGGCGCAAGCCTGAT	372
Db	296	GAGTCACGACTCTTACCGGAGGACGACAGTGGGAAATATTGACATATGGGCGCAAGCCTGAT	355

QY	372	CCAGCCAGCCCGCGTGTGAAGAAAGGCTTAAAGGTTGTAAGCACTTTCACAGGGTAGG	432
Db	356	CCAGCCATGCCCGCGTGTGAAGAAAGCTTCGGAATTGTAAAGCACTTTAACTTTGGAGG	415
QY	433	AAAGGTGATGAGTTAATACGTTATCATCTTGACGTTAGCCCAAGAAAGCACCGGCTAA	492
Db	416	AAAGGATTAATACCTAATACGTTAGTGTGTTTGAAGTTACGACAGATAAAGCACCGGCTAA	475
QY	493	CTCTGCGCAGAGCCCGGGTAAATACAGAGGCGCAAGCGTTAATCGGAATTATCTGGGCG	552
Db	476	CTCTGTGCCAGAGCCCGGGTAAATACAGAGGCGCAAGCGTTAATCGGAATTATCTGGGCG	535
QY	553	TAAAGCGCGTAGGTGGTTGTTAACTCGGATGTGAATATCCAGGGCTCAACCTTGGAA	612
Db	536	TAAAGCGCGTAGGTGGTTGTTAACTCGGATGTGAATATCCAGGGCTCAACCTTGGAA	595
QY	613	TGGCACCCGATCTCGGCTAGCTAGATGATGTTAGAGGGGTGTGGAATTTCCGTGTACG	672
Db	596	CTGCATCAAACTGACACAGCTAGATGATGTTAGAGGGGTGTGGAATTTCCGTGTACG	655
QY	673	GTGAATGCGTAGATATATAGAAAGAACATCAGTGTGTGAAGCGACACCTGTGACTAATAC	732
Db	656	GTGAATGCGTAGATATATAGAAAGAACACATGCGGAAGCGACACCTGTGACTAATAC	715
QY	733	TGACACTGAGGTGGGAAAGCGTGGGGAGCAAAACAGATTAGATACCTGTGTGTACAGC	792
Db	716	TGACACTGAGGTGGGAAAGCGTGGGGAGCAAAACAGATTAGATACCTGTGTGTACAGC	775
QY	793	CGTAAACGATGTCTAAGCCGTTGG--GTTGTAACTGACTTAATGTGGCGAGCTAACGCA	850
Db	776	CGTAAACGATGTCTAAGCCGTTGGAGGAGCCTTGAACCTTGTGTGTGGCGAGCTAACGCA	835
QY	851	TAAAGTAGACCGCTGGGGAGATACGGCCGCAAGGTCTAAACTCAATATGATTTGACGGGCG	910
Db	836	TAAAGTAGACCGCTGGGGAGATACGGCCGCAAGGTCTAAACTCAATATGATTTGACGGGCG	895
QY	911	CCGCAACAGCGGTGAGCATGTGGTTAATTCGAGCAACGCGAAGAACCTTACTACTC	970
Db	896	CCGCAACAGCGGTGAGCATGTGGTTAATTCGAGCAACGCGAAGAACCTTACTACTC	955
QY	971	TTGACACTCACAGAACATTATAGAGATCAGATGTCCTTCGGGAACTGTGACAGGTG	1030
Db	956	TTGACACTCACAGAACATTTCAGAGATGATGTGGTGTCTTCGGGAACTGTGACAGGTG	1015
QY	1031	CTGCATGCGTGTCTGCACTTCGTGTGTGAATGTTGGGTTAAGTTCGCTAACGAGCGCA	1090
Db	1016	CTGCATGCGTGTCTGCACTTCGTGTGTGAATGTTGGGTTAAGTTCGCTAACGAGCGCA	1075
QY	1091	ACCCATTGCTCTAATTTGCGACAGATATGTGTGGGAACTTTAAGAGACCTGCGGTGACA	1150
Db	1076	ACCCATTGCTCTAATTTGCGACAGATATGTGTGGGCACTCTAAGAGACCTGCGGTGACA	1135
QY	1151	AACCGAGAGAGGTGGGAGCAGCGTCGTAAGTCATGTGCGCTTTACGAGTAGAGGCTTACCA	1210
Db	1136	AACCGAGAGAGGTGGGAGTAGCTCAAGTCATCATGTGCGCTTTACGAGTAGAGGCTTACCA	1195
QY	1211	CGTGCATCAATGGCGTATATACAGAGGTGTGAAGCTATGTGAGCGCAATCCCAACAA	1270
Db	1196	CGTGCATCAATGGTGTGTACAGAGGTTGTCCAAAGCCGCGAGGTGAGCTAATCCCAACAA	1255
QY	1271	GTACGTCGTAATCCGATTTGAGATCTTGCAACTGCACTGCATGAAAGTCGTAAGT	1330
Db	1256	ACCGATCGTAATCCGATTCGAGATCTGCAACTGCACTGCGTGAAGTCGTAATTCGTAAGT	1315
QY	1331	ATGCGTAATCAAGATGTACAGGTAAATACGTTCCCGGCGCTTGTACACACCGCCGCTAC	1390
Db	1316	ATGCGTAATCAAGATGTGCGGTAAATACGTTCCCGGCGCTTGTACACACCGCCGCTAC	1375
QY	1391	ACCATGGAATGATGTGCTCCAGAAAGTAGTACCTTAACCTTCGAGGAGTGGCGGTATCC	1450
Db	1376	ACCATGGAATGATGTGCTCCAGAAAGTAGTACCTTAACCTTCGAGGAGCGGTATCC	1433

QY 1451 ACGAGTGTCAATGATGAGTGTGAAGTCTAC 1483
Db 1434 ACGGTGTATTCATGACTGAGGATGATGCTAC 1466

RESULT 5

US-08-114-695A-6
Sequence 6, Application US/08114695A
Patent No. 5508193
GENERAL INFORMATION:
Applicant: Mandelbaum, Raphael T.
TITLE OF INVENTION: DEGRADATION OF S-TRIAZINES IN SOIL AND
TITLE OF INVENTION: WATER
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCHWEMAN, LUNDBERG & MOESSNER, P.A.
STREET: 3500 IDS CENTER
CITY: MINNEAPOLIS
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/114,695A
FILING DATE: 31-AUG-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MUEHLING, ANN M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 600,268US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1518 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: rRNA
ORIGINAL SOURCE:
ORGANISM: Pseudomonas aeruginosa
US-08-114-695A-6

Query Match 74.7%; Score 1109.4; DB 1; Length 1518;
Best Local Similarity 69.0%; Pred. No. 0;
Matches 1023; Conservative 258; Mismatches 192; Indels 9; Gaps 6;
QY 3 TAGCTCAATGAAAGCTGCGGAGGCTTAAACATGCAATGCGAGCGTAAACAGGG 62
Db 20 UGGUCUAGAUUGAACGUCGCGGAGGCGUAAACAUGCAAGUCAGAGCG-AUGAAGG 78
QY 63 AGTTGCTCTGCTGACGAGCGGCGGAGCGGTAGTAAAGCGGTAGGATCTCTCTAG 122
Db 79 AGCTGCTCTGCTGACGAGCGGCGGAGCGGTAGTAAAGCGGTAGGATCTCTCTAG 137
QY 123 AGGGGGAACAATGTAAGACGATGCTATACCGGATCGCCCTGAGGGGGAAGAGG 182
Db 138 UGGGGGAUAAGUCUGGAAACGCGGCGUAAUACCGCAUACGUCUCUAGGGAAGAGGGG 197
QY 183 GGACTCTTCGAGGCTTCGCTATTAGATGAGGCTCGGATTAAGTTAGTTGAGGG 242
Db 198 GGAUCCU--CGAACUCUACGCUAUCNAGUAGCCUAGGUCGAGUUVAGUAGUGAGG 255
QY 243 TAAAGGCTACCAAGGAGAGATCTCTAATGCTGAGAGAGATGACAGTCACTGG 302
Db 256 UAAAGGCCUACCAAGGAGAGATCTCTAATGCTGAGAGAGATGACAGTCACTGG 315

QY 303 ACTGAAACACGCGCCAGATCTCTACGAGAGGAGCAAGTGGGAAATTGGACATGCGC 362
Db 316 ACTGAAACACGCGCCAGATCTCTACGAGAGGAGCAAGTGGGAAATTGGACATGCGC 375
QY 363 CAAGCTGATCCAGCCATGCGCGTGTGAGAGAGGCGCTTGGAGTTGTAAGCACTTC 422
Db 376 AAGCCNGAUCAGCCATGCGCGTGTGAGAGAGGCGCTTGGAGTTGTAAGCACTTC 435
QY 423 AGGGGTGAGAGAGGATGATGATTAATACCTTATCTTGAAGTCCAGAGAGAG 482
Db 436 AGUUGAGAGAGAGGAGAGATGATTAATACCTTATCTTGAAGTCCAGAGAGAG 495
QY 483 CACCGCTACTGTGAGAGAGAGGAGGATTAACAGAGGATGAGAGGATTAACAGAG 542
Db 496 CACCGCTACTGTGAGAGAGAGGAGGATTAACAGAGGATGAGAGGATTAACAGAG 555
QY 543 TTAAGGAGGATTAAGGAGGAGGATGATGATGATGATGATGATGATGATGATG 602
Db 556 UTAAGGAGGATTAAGGAGGAGGATGATGATGATGATGATGATGATGATGATG 615
QY 603 AACCTGGAATGAGCAACCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 662
Db 616 AACCTGGAATGAGCAACCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 675
QY 663 CTGTGTAGGAGGATTAAGGAGGATTAAGGAGGATTAAGGAGGATTAAGGAGGAT 722
Db 676 CTGTGTAGGAGGATTAAGGAGGATTAAGGAGGATTAAGGAGGATTAAGGAGGAT 735
QY 723 GGAATTAATCTGACTGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 782
Db 736 GGAATTAATCTGACTGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 795
QY 783 TAGTCCAGCGGTAACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Db 796 TAGTCCAGCGGTAACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 855
QY 841 GCTAACGAAATGATGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Db 856 GCTAACGAAATGATGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 915
QY 901 TGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 960
Db 916 TGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 975
QY 961 TTAAGTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
Db 976 TTAAGTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1035
QY 1021 GAGACAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1080
Db 1036 GAGACAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1095
QY 1081 AAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1140
Db 1096 AAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1154
QY 1141 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200
Db 1155 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1214
QY 1201 GGGCTACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1260
Db 1215 GGGCTACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1274
QY 1261 ATCCCAAAAGTACGTCGATGATGATGATGATGATGATGATGATGATGATG 1320
Db 1275 ATCCCAAAAGTACGTCGATGATGATGATGATGATGATGATGATGATGATG 1334
QY 1321 ATGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380
Db 1335 ATGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1394
QY 1381 CGCCGCTACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1440

RESULT 8

US-08-520-946-158

/ Sequence 158, Application US/08520946
/ Patent No. 6372424

GENERAL INFORMATION:

/ APPLICANT: BROW, MARY ANN D.
/ APPLICANT: LYAMICHEV, VICTOR I.

/ APPLICANT: OLIVE, DAVID M.

/ TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
/ PATHOGENS

/ NUMBER OF SEQUENCES: 160

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: MEDLEN & CARROLL

/ STREET: 220 MONTGOMERY STREET, SUITE 2200

/ CITY: SAN FRANCISCO

/ STATE: CALIFORNIA

/ COUNTRY: UNITED STATES OF AMERICA

/ ZIP: 94104

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ COMPUTER: IBM PC compatible

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: Patentin Release #1.0, Version #1.25

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/08/520.946

/ FILING DATE:

/ CLASSIFICATION: 435

/ ATTORNEY/AGENT INFORMATION:

/ NAME: CARROLL, PETER G.

/ REGISTRATION NUMBER: 32,837

/ REFERENCE/DOCKET NUMBER: FORS-01756

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: (415) 705-8410

/ TELEFAX: (415) 397-8338

/ INFORMATION FOR SEQ ID NO: 158:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 1542 base pairs

/ TYPE: nucleic acid

/ STRANDEDNESS: double

/ TOPOLOGY: linear

/ MOLECULE TYPE: DNA (genomic)

US-08-520-946-158

Query Match

Best Local Similarity 71.6%; Score 1064.6; DB 4; Length 1542;

Matches 1266; Conservative 0; Mismatches 199; Indels 12; Gaps 7;

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QY 3 TAGCTCAGATTGAGCGCTGGCGGCGAGCTTAAACACATGCAAGTCGACGGGTAAACAGG-- 60
DB 20 TGGCTCAGATTGAGCGCTGGCGGCGAGCTTAAACACATGCAAGTCGACGGGTAAACAGGAA 78
QY 61 GGAGCTTGCTCC-TGCTGACGAGCGGCGGAGCGGCTGATGTAACGCGTAGAATCTGCTTA 118
DB 79 GAAGCTTGCTCTTGCTGACGAGTGCGGAGCGGCTGATGTAATGCTGCGAAACTGCTG 138
QY 119 ATGAGAGGCGGACAAATGGAATGGAACGATGCTAATACCGCATAGCCCTGAGGCGGAAAG 178
DB 139 ATGAGAGGCGGATTAATCTGGAACGATGCTAATACCGCATAGCCCTGAGGCGGAAAG 198
QY 179 GAGGGAAGCTTCGAGAGCTTCGCTATTAGTAGAGCTGCGTAGAATTGACTAGTGT 238
DB 199 AGGCGGGA--CTTCGCGGCTCTTGCCATCGGATGCGCCAGATGAGATTGCTAGTGT 256
QY 239 AGGCTAAAGCTTACCAAGGCGACGATCTTAACCTGCTGAGAGATGACAGTCAAC 298
DB 257 GAGGTAAAGCTTACCAAGGCGACGATCTTAACCTGCTGAGAGATGACAGTCAAC 316
QY 299 TGGGACTGAGACACGCGCAGACTCTACGAGGAGCAGACAGTGGGGAATATTGACATG 358
DB 317 TGGACTGAGACACGCGTCAAGCTCTACGAGGAGCAGACAGTGGGGAATATTGACATG 376
QY 359 GGGCGAAGCTTGATCCAGCATGCGCGTGTGTGAAGAAGCTTAGGTTGTAAAGCAC 418
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DB 377 GCGCAAGCTGATGACGCAATGCCGCTGTATGAAGAAGGCTTGGGTTGTAAAGTAC 436
QY 419 TTTCAGAGGTGAGAGAGGTGATAGTTAATACGTTATCATCTTGAACGTTAGCCCGAGA 478
DB 437 TTTCAGAGGTGAGAGAGGTGATAGTTAATACGTTATCATCTTGAACGTTAGCCCGAGA 496
QY 439 GAAGCACCAGGCTAATCTGTGCCAGACCGCGGTAAATACAGAGGCTGAGAGGTTAAAC 538
DB 497 GAAGCACCAGGCTAATCTGTGCCAGACCGCGGTAAATACAGAGGCTGAGAGGTTAAAC 556
QY 539 GGAATTACTGAGCGTAAAGCGCGAGTGTGTTGTAACTGAGATGTGAATCCAG 598
DB 557 GGAATTACTGAGCGTAAAGCGCGAGTGTGTTGTAACTGAGATGTGAATCCAG 616
QY 599 GCTCACTTGGAATGGCACCCCATCTGCTAGCTAGATGTAGTAGAGGCTGTGGA 658
DB 617 GCTCACTTGGAATGGCACCCCATCTGCTAGCTAGATGTAGTAGAGGCTGTGGA 676
QY 659 TTTCCTGTGAGCGGTGAATGCGTATGATGAAGAACAATCATGTCGCGAGCGAGA 718
DB 677 TTTCAGAGGTGAGAGAGGTGATAGTTAATACGTTATCATCTTGAACGTTAGCCCGAGA 736
QY 719 CCTGGAATTAATCTGACATCTGAGTGCAGAAAGCTGGGAGCAACAGATTAATACC 778
DB 737 CCTGGAATTAATCTGACATCTGAGTGCAGAAAGCTGGGAGCAACAGATTAATACC 796
QY 779 CTGATGATCCAGCGCGTAAAGCGATGCTACTAGCCG--TTGGGTTATGACTTAGTGC 836
DB 797 CTGATGATCCAGCGCGTAAAGCGATGCTACTAGCCG--TTGGGTTATGACTTAGTGC 856
QY 837 CGCAGCTTAACGCAATTAATGAGACCGCTGGGAGTACCGCGCAAGTTAAATCTCAAT 896
DB 857 CGCAGCTTAACGCGTTAATGAGACCGCTGGGAGTACCGCGCAAGTTAAATCTCAAT 916
QY 897 GAATTGACGGGCGCGGACAAAGCGGTGAGAGATGAGTTAATGGAAGCAAGCGAAG 956
DB 917 GAATTGACGGGCGCGGACAAAGCGGTGAGAGATGAGTTAATGGAAGCAAGCGAAG 976
QY 957 AACCTTAATCTGATCTTACATCCACAGAAATTTGAGAGATGAGTGTGCTGGGAA 1016
DB 977 AACCTTAATCTGATCTTACATCCACAGAAATTTGAGAGATGAGTGTGCTGGGAA 1036
QY 1017 CTGGAAGACAGTGTGCTGATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1076
DB 1037 CTGGAAGACAGTGTGCTGATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1096
QY 1077 CCGTAACGAGCGCAACCTTGTCTTATTTGCCAGACGTAATGCTGGGAACCTTTAAGCA 1136
DB 1097 CCGTAACGAGCGCAACCTTGTCTTATTTGCCAGACGTAATGCTGGGAACCTTTAAGCA 1155
QY 1137 GACTGCGGTGACAAACCGAGAGAGGTGGGAGCAACCTTAATGCTATGCTGCTTACG 1196
DB 1156 GACTGCGGTGACAAACCGAGAGAGGTGGGAGCAACCTTAATGCTATGCTGCTTACG 1215
QY 1197 AGTAGGGGTACACAGCTGCTACATAGGCGTATACAGAGGCTGCAAGCTTAGCATAGTA 1256
DB 1216 AOCAGGGGTACACAGCTGCTACATAGGCGTATACAGAGGCTGCAAGCTTAGCATAGTA 1275
QY 1257 GCGAATCCACAAAGTACGTGTGATGCTGCGATTGAGAGTCTGCACTGACTCATTAAGT 1316
DB 1276 GCGAATCCACAAAGTACGTGTGATGCTGCGATTGAGAGTCTGCACTGACTCATTAAGT 1335
QY 1317 GCGAATGCTAGTAATGCTGAATCAGAAATGCAAGGTGAATAGCTTCCGGGCGCTGTAC 1376
DB 1336 GCGAATGCTAGTAATGCTGAATCAGAAATGCAAGGTGAATAGCTTCCGGGCGCTGTAC 1395
QY 1377 ACACCGCCGCTCACACCAATGAGAGTATTGCTTCAGAAATGACTTACCTTTCCG 1436
DB 1396 ACACCGCCGCTCACACCAATGAGAGTATTGCTTCAGAAATGACTTACCTTTCCG 1453
QY 1437 GGAATGGGCTTACCAAGAGAGTGTCAATGACTGAGGAGT 1473
DB 1454 GGAATGGGCTTACCAAGAGAGTGTCAATGACTGAGGAGT 1490
```

RESULT 9

US-08-114-695A-1

Sequence 1, Application US/08114695A

Patent No. 5508193

GENERAL INFORMATION:

APPLICANT: Mandelbaum, Raphael T.

TITLE OF INVENTION: DEGRADATION OF S-TRIAZINES IN SOIL AND

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCHWEGMAN, LUNDBERG & WOESSNER, P.A.

STREET: 3500 IDS CENTER

CITY: MINNEAPOLIS

STATE: MN

COUNTRY: USA

ZIP: 55402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/114,695A

FILING DATE: 31-AUG-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MOETING, ANN M.

REGISTRATION NUMBER: 33,977

REFERENCE/DOCKET NUMBER: 600,268US1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 612-339-0331

TELEFAX: 612-339-3061

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1542 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: rRNA

ORIGINAL SOURCE:

ORGANISM: Escherichia coli

US-08-114-695A-1

Query Match 71.3%; Score 1058.8; DB 1; Length 1542;
Best Local Similarity 68.3%; Pred. No. 0;
Matches 1009; Conservative 248; Mismatches 207; Indels 14; Gaps 6;

3 TAGCTCAGATTGAACGCTGCGGCGAGCTTAACACATGCAAGTCGAGCGGTAAACAGGG 62
20 UGGCUCACAGUUAAGCGUGCGGCGAGGCGU-ACACAUAGCAAGCGUAAACAGGA 78
63 AGCTGCTCC-----TGCTGACGAGCGGCGGAGTACGCGTACGCGTACGCGT 117
79 AGAAGCTUCUCUCUUGGACGAGUGGCGGAGCGGAGUAGUAGUCUGGAGAAACGCGCU 138
118 AGTAGAGGAGCAACATGTGAAACGATGCTAATACCGCATACGCGCTGAGGGGAGAA 177
139 GAUGAGGGGGGUAACUACUGGAAACGUAUACCCCAUAAAGUCGACACCAAG 198
178 GAGGGGAGCTCTTCCGAGACCTTCCGCTATTAGTAGACCTGCGGTGAGATTAGTAATGG 237
199 AGGGGG--ACCUUGGGGCGUCUUGCCAUUCGAGUGGCCCAAGUUGGAGUUAAGCUAUAAG 255
238 TAGGTAAGGCTTACCAAGGCGAGATCTCTAAGTGTGAGAGATGACCAATGAC 297
256 UGGGUAACGGCUCACCUAAGCGAGAGUCCUAGUCUGUAGAGAUACAAGCAACA 315
298 CTGGGACTGAGACACGCGCCGACTCTTACGCGAGGCGAGAGTGGGGATATTGGCAAT 357
316 CUGGAACUGAGACACGCGUCACACUCCUACGCGAGGCGAGAGUGGGAGAAUUAUUGCAAAU 375

358 GGGCGCAAGCCTGATCCAGCCATGCCCGCTGTGTGAGAAGGCTTAGGTTGTAAGA 417
376 GGGCGCAAGCCTGATCCAGCCATGCCCGCTGTGTGAGAAGGCTTAGGTTGTAAGA 435
418 CTTTCAGAGGTGAGAAAGGTGATGATTATATGATATCATCTTACCTTAGACCCGAGA 477
436 CUUUCACGGGGAGAGAAAGGAGUAAAGUUAUACCUUUCUACUUGACUUAACCCGACAA 495
478 AGAAGCACCGGCTTACTCTGTCCAGACGCCCGGTAAATACAGAGGTTCCAAAGCTTAAT 537
496 AGAAGCACCGGCTTACTCTGTCCAGACGCCCGGTAAATACAGAGGTTCCAAAGCTTAAT 555
538 CGAATTACTGAGGCTTAAAGCGCGGTAGGTTTAAAGCGGATGTAATCCGAG 597
556 CGAATUUAUUGGGGUAAGCGGACCGAGCGGUGUUAUUGUUAUUGUUAUUGUUAUUG 615
598 GGTCAACCTTGAAATGGCAACCGGATCTGCTAGCTAGTATGATAGGAGGGGTGGA 657
616 GGTCAACCTTGAAATGGCAACCGGATCTGCTAGCTAGTATGATAGGAGGGGTGGA 675
658 ATTTCCTGTAGCGGTGAAATGCGTATATGAAAGGAACATCATGTCGCGAAGCGAC 717
676 AUTCAGAGUUAAGGUGUAAUAGCGUAGAUUCGAGAUUAACGUGGCGAAGGCGGC 735
718 ACCCTGACTAATATCTGACACTGAGGTGCGAAAGCGTGGGAGCAAAACAGATTAGATAC 777
736 CCCUGAGCAAGATGUAACGCTUAGGUGGAAAGCGGAGGAGCAAAACAGAUUAGUAC 795
778 CTTGTAGTCCAGCGCTTAAAGATGCTTAAAGCGG- TTGGGTTGTAATGACTTAGTC 835
796 CCUGGUGUUAAGCGGUAACGUAUAGCGUAGAUUCGAGAUUAUUGUUAUUGUUAUUG 855
836 GCGAGCTTAAAGCAATGATGAGACCGCTGAGGAGTACCGCGCAAGGTTAAACTCAAA 895
856 CCGAGGCUAAACGCGUUAAGCGUUAAGCGGCTGAGGAGUACCGCGCAAGGUAUUAACAA 915
896 TGAATTGACGGGAGCGCGCAAGCGGTGAGCATGTGTTAATTGAAAGCAGCGGA 955
916 UGAUUAUAGCGGAGCGCGCAAGCGGUGAGAUUGUUAUUGUUAUUGUUAUUGUUAUUG 975
956 GAACCTTACCTAATCTTGAATGACAGAAACATTGAGAGATCAGATGATGCTTCCGGA 1015
976 GAACCTTACCTAATCTTGAATGACAGAAACATTGAGAGATCAGATGATGCTTCCGGA 1035
1016 ACTGTGAGACAGGTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1075
1036 ACCGUGAGACAGGTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1095
1076 CCGGTAACGAGCGCAACCTTGTCTTATTGTCGACAGCTAATGCTGGAACCTTAAAG 1135
1096 CCGGTAACGAGCGCAACCTTGTCTTATTGTCGACAGCTAATGCTGGAACCTTAAAG 1154
1136 AGACTGCGGTGACAAACCGGAGAGTGGGAGCAGACTCAAGTCAATCATGAGCCCTTAA 1195
1155 AGACTGCGGTGACAAACCGGAGAGTGGGAGCAGACTCAAGTCAATCATGAGCCCTTAA 1214
1196 GAGTAGGCTTACACAGCTGCTTACATGCGGTATACAGAGGCTGCAAGCTTACGATATG 1255
1215 GACGAGGCTTACACAGCTGCTTACATGCGGTATACAGAGGCTGCAAGCTTACGATATG 1274
1256 AGGGAATCCGCAAAAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1315
1275 AGGGAATCCGCAAAAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1334
1316 TCGGAATCGTATGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1375
1335 UCGGAATCGTATGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1394
1376 CACACGCGCGCTGACACCAAGTGGGAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1435
1395 CACACGCGCGCTGACACCAAGTGGGAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1452

QY 1436 GGGATGCGGCTTACACGAGTGTCAATGACTGGGCT 1473
DB 1453 GGGAGGGCGCUACACCUUGUGAUCAGACUGGGGU 1490

RESULT 10

US-08-632-470-53

Sequence 53, Application US/08632470

Patent No. 5976791

GENERAL INFORMATION:

APPLICANT: MABILAT, CLAUDE

APPLICANT: RAOULT, DIDIER

TITLE OF INVENTION: NUCLEOTIDE FRAGMENTS CAPABLE OF

HYBRIDIZING SPECIFICALLY TO RICKETTSIA PUNA OR RENA AND

TITLE OF INVENTION: THEIR USE AS PROBES OR PRIMERS

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: OLIFF & BERRIDGE

STREET: P.O. BOX 19928

CITY: ALEXANDRIA

STATE: VA

COUNTRY: USA

ZIP: 22320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/632,470

FILING DATE: 08-JUL-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: BERRIDGE, WILLIAM P

REGISTRATION NUMBER: 30,024

REFERENCE/DOCKET NUMBER: WPB 38238

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)-836-6400

TELEFAX: (703)-836-2787

INFORMATION FOR SEQ ID NO: 53:

SEQUENCE CHARACTERISTICS:

LENGTH: 1484 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-632-470-53

Query Match 71.2%; Score 1057.4; DB 2; Length 1484;

Best Local Similarity 84.9%; Pred. No. 0;

Matches 1248; Conservative 0; Mismatches 212; Indels 10; Gaps 6;

QY 3 TAGCTCAGATTGAACGCTGCGCAGGCTTAAACACATCAAGTCGAGCGGTA--CAGG 60
DB 20 TGGCTCAGATTGAACGCTGCGCAGGCTTAAACACATCAAGTCGAGCGGTA--CAGG 78
QY 61 GAGACTGCTCTGCTGCTACGAGC--GGCGGACGGGTGAATACGGGTAGAGATTCGCTTA 118
DB 79 GAGCTTCTCTGCGCGGCGAGAGTGGCGGAGCGGTGAATACGGGTAGAGATTCGCTTA 138
QY 119 GTAGAGGGGACCAACATGTGAAACGATGCTAATACCGCATACGCGCTGAGGGGAAAG 178
DB 133 GTAGTGGGGGTAACCTGGGAAACTCGGCTAATACCGTATATCTTTGGACAAAG 198
QY 179 GAGGGGACTCTTGGAGCCTTCGCTATTTAGATGAGCCTGCGTGAATTTAGTATGCT 238
DB 199 CGGGGGA--TCTTGGACCTCTGCTATTAAGATGAGCCTACGCTGATTTAGCTTTGCT 256
QY 239 AGGTAAGGCTTACCAAGGCGACGATCTCTAATGCTGTGAGAGATGACCACTACAC 298
DB 257 GGGTAAATGGCTTACCAAGGCGACGATCTCTAATGCTGTGAGAGATGACCACTACAC 316
QY 299 TGGGACTGAGACACGCGCCCACTCTTACGGGAGGACGAGTGGGGATATTGGACAATG 358

DB 317 TGGGACTGAGACACGCGCCCACTCTTACGGGAGGACGAGTGGGGATATTGGACAATG 376
QY 359 GGGCAAGCCTGATCAGGCATGCCGCTGTGTGAAGAAGCCTTAGGTTGTAAAGCAC 418
DB 377 GGGGAAACCCTGATCAGCAATGCCGCTGTGTGAAGAAGCCTTAGGTTGTAAAGCAC 436
QY 419 TTTGAGGGGTGAGAAAGGTGATAGTTTAATACGTATCATCTTGACCTTAGCCCGGAA 478
DB 437 TTTGGGTGGGAAAGAAATTTCTCAAGGTAATATCTTGGCGTTGACGTTACCAAGAA 496
QY 479 GAAGCACCGCTAATCTGTGCGACAGCCCGGTAAATACAGAGGTGCAAGCCTTAATC 538
DB 497 GAAGCAGCTGCTAATCTGTGCGACAGCCCGGTAAATACAGAGGTGCAAGCCTTAATC 556
QY 539 GGAATTAATCTGGCGCTAAAGCGCGCTAGGTGTTTGTAACTGCAATGTAATCCAG 598
DB 557 GGAATCACTGGCGCTAAAGCGCGCTAGGTGTTTGTAACTGCAATGTAATCCAG 616
QY 599 GCTCAACCTTGGATGCGACCCGATCTAGCTAGTATGATGTAGAGGGGTGAGAA 658
DB 617 GCTNNCTGGGAAATTTGACCCGATCTAGCTAGTATGATGTAGAGGGGTGAGAA 676
QY 659 TTTCTGTGTAGCGGTGAATGCTGATATATGAGAGGAATCATGTCGCAAGCCACA 718
DB 677 TTTCCGCTGTAGCGGTGAATGCTGATATATGAGAGGAATCATGTCGCAAGCCACT 736
QY 719 CCTGGAATTAATACGACCTGAGAGGTGGAAGGCTGGGGAGCAACAGATTAATATAC 778
DB 737 TCTTGACCAATTAATACGACCTGAGAGGTGGAAGGCTGGGGAGCAACAGATTAATAC 796
QY 779 CTGATGTCAGCGCGGTAAACGATGTCTACTAGCGGTGAGTGG--TATGACTTATGTC 837
DB 797 CTGATGTCAGCGCGGTAAACGATGTCTACTAGCGGTGAGTGG--TATGACTTATGTC 856
QY 838 GAGCTTAAGCAATATAGTACGCGCTGGGAGTACCGCCGCAAGTTAACTCAATG 897
DB 857 GAGCTTAAGCAATATAGTACGCGCTGGGAGTACCGCCGCAAGTTAACTCAATG 916
QY 898 AATTGACGGGGCCCGCAACAGCGGTGAGGATGTTTAACTGAAAGCAACCGGAGA 957
DB 917 AATTGACGGGGCCCGCAACAGCGGTGAGGATGTTTAACTGAAAGCAACCGGAGA 976
QY 958 AACTTAATCTTCTGACATCCAGCAACATTTGAGAGTATGATGCTTCGGGAC 1017
DB 977 AACTTAATCTTCTGACATCCAGCAACATTTGAGAGTATGATGCTTCGGGAC 1036
QY 1018 TGTGACAGAGTGTGATGAGGCTGTCAGCTGCTGTTGAAATGTTGGTTAATGCC 1077
DB 1037 CGAGTACAGAGTGTGATGAGGCTGTCAGCTGCTGTTGAAATGTTGGTTAATGCC 1096
QY 1078 CGTACGACGCAACCTTGTCTTATTTGCAAGCACTAATGTTGGGAACTTTAAGAG 1137
DB 1097 CGTACGACGCAACCTTGTCTTATTTGCAAGCACTAATGTTGGGAACTTTAAGAG 1156
QY 1138 ACTGCGGTGACAAACCGGAGGAAGTGGGGACGACGTCAAGTATCATGCGCTTGA 1197
DB 1157 ACTGCGGTGACAAACCGGAGGAAGTGGGGACGACGTCAAGTATCATGCGCTTGA 1216
QY 1198 GTAGGGCTACACGCTGCTCAATGCGTATATCAAGGGCTGCAAGCTTAGGATAGT 1257
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DB 1277 CTAATCCGCAAGTACGTCGATGAGTCCGATTTGAGTGTGCACTGCACTCATGAATC 1336
QY 1318 GGAATGCTAGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 1377
DB 1337 GGAATGCTAGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 1396
QY 1378 CACCGCGGTGACCAATGAGGATGATTTGCTCCAGAAAGTATGCTTAACCTTGGAG 1437

Db 1315 CGGTGAATAGCTTCCCGGGCCCTTGTACACACCCCGCTCACACCATGGAGTTATCTCA 1374
 QY 1410 CCAGAGTAGCTAGCTTACCCCTTGGGGATGGCGGTACACCGAGAGGTCAATGACTG 1469
 Db 1375 CCAGAGTGTGTTAGCTTACCGC---AAGAGGCGCATCACACGGTGGGTGCTGACTG 1430
 QY 1470 GGGT 1473
 Db 1431 GGGT 1434

RESULT 12
 US-09-228-184-1
 ; Sequence 1, Application US/09228184
 ; Patent No. 6322782
 ; GENERAL INFORMATION:
 ; APPLICANT: WALKER, Harrell L.
 ; APPLICANT: HIGGINBOTHAM, Lawrence R.
 ; TITLE OF INVENTION: CONTROL OF CYANOBACTERIA WITH A BACTERIUM
 ; FILE REFERENCE: 013243-0007
 ; CURRENT APPLICATION NUMBER: US/09/228,184
 ; NUMBER OF SEQ ID NOS: 1
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 1540
 ; TYPE: DNA
 ; ORGANISM: Unknown Organism
 ; FEATURES:
 ; OTHER INFORMATION: Description of Unknown Organism: Bacterium SG-3;
 ; OTHER INFORMATION: gram negative; rod-shaped; exhibits flagellae;
 ; OTHER INFORMATION: motility; pathogenic to cyanobacteria and algae;
 ; OTHER INFORMATION: yellow colonies on BG-11 medium suppl. with tryptic
 US-09-228-184-1

Query Match 69.2%; Score 1028.2; DB 4; Length 1540;
 Best Local Similarity 83.7%; Pred. No. 0;
 Matches 1238; Conservative 0; Mismatches 228; Indels 13; Gaps 6;

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 QY 63 AGCT---TCTCTCTCTGACGAGCGGCGGAGGTGAGTAACGCTGAGTAATCTGCTA 118
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 QY 119 GTGAGGGGGGCAACAATGTGGAACGCAATGCTTAATACCGCATACGCTTGAAGGGAAG 178
 Db 135 GTGAGGGGGGCAACAATGTGGAACGCAATGCTTAATACCGCATACGCTTGAAGGGAAG 194
 QY 179 GAGGGAGCTCTTGGAGGCTTGGAGTATGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 238
 Db 195 GAGGGAG--TCGGAACCTTGGAGGCTTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 252
 QY 239 AGGGTAAAGGCTTACCAAGGCGAAGCTTCTTAATCTGAGTGGAGTGGAGTGGAGTGGAGT 298
 Db 253 GGGGTAAAGGCTTACCAAGGCGAAGCTTCTTAATCTGAGTGGAGTGGAGTGGAGTGGAGT 312
 QY 299 TGGAGCTGAGACAGCGGCCAGACTCTTACGAGAGGAGAGAGTGGAGTGGAGTGGAGTGGAGT 358
 Db 313 TGGAGCTGAGACAGCGGCCAGACTCTTACGAGAGGAGAGAGTGGAGTGGAGTGGAGTGGAGT 372
 QY 359 GGGCGAAGCTTATCCAGCGATGCGGTGTGTAAGAAAGCTTAAAGGCTTAAAGAAC 418
 Db 373 GGGCGAAGCTTATCCAGCGATGCGGTGTGTAAGAAAGCTTAAAGGCTTAAAGAAC 432
 QY 419 TTTTCAAGGGTGAAGAGGGTATGATGATATGATATGATATGATATGATATGATATGATATGATAT 478
 Db 433 TTTTGTCCGAAAGAAAGAAAGCACTGATTAATCTTCTGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 492
 QY 479 GAAGCAACGGCTACTCTGTGTCAGAGACCGCGGTAAATACAGAGGGTGCAGAGCTTAATC 538

Db 493 TAAGACCGGCTAATCTTCTGTCAGACAGCCGCGGTAAATAGAAAGGGTGCAGAGGTTACTC 552
 QY 539 GGAATTACTGGGCGCTAAAGCGCGGTAGGTGTTGTTAGTGGATGTAATCCAGG 598
 Db 553 GGAATTACTGGGCGCTAAAGCGCGGTAGGTGTTGTTAGTGGATGTAATCCAGG 612
 QY 599 GCTCAACCTTGAATGGCAACCGGTAAGTGGCTGATGATGATGATGATGATGATGATGATGAT 658
 Db 613 GCTCAACCTTGAATGGCAACCGGTAAGTGGCTGATGATGATGATGATGATGATGATGATGAT 672
 QY 659 TTTCTGTGTCAGCGGTGAAATGCTGATATGAGAAAGCAATCAATGAGGAGGAGGAGCA 718
 Db 673 TTTCTGTGTCAGCGGTGAAATGCTGATATGAGAAAGCAATCAATGAGGAGGAGGAGC 732
 QY 719 CCTTGAATTAATGACTGACATGAGGTGCGAAAGCGTGGGAGGCAACAGATTAATACC 778
 Db 723 ATCTGACACAGACTGACATGAGGTGCGAAAGCGTGGGAGGCAACAGATTAATACC 792
 QY 779 CTGTAATGTCACCGCGTAAAGATGCTACTAGCCGTGGGT---TGTATGCTTAATG 835
 Db 793 CTGTAATGTCACCGCGTAAAGATGCTACTAGCCGTGGGT---TGTATGCTTAATG 852
 QY 836 GCGCAGCTAACGCAATAGTAGACCGGCTGGGAGTACGCGCCGCAAGGTTAAACTCAA 895
 Db 853 TCGAAGCTAACGCGTTAGTTCGCGCTGGGAGTACGCGCCGCAAGCTGAACCTCAA 912
 QY 896 TGAATTAAGCGGGGCGCGCAACAGCGGTGAGCATGTGTTAATGGAAGCAACCGAA 955
 Db 913 GGAATTAAGCGGGGCGCGCAACAGCGGTGAGCATGTGTTAATGGAAGCAACCGAA 972
 QY 956 GAACCTTACTACTCTTGAACATCCACAGAACTTGAAGATGAGTGGTGGGGA 1015
 Db 973 GAACCTTACTACTCTTGAACATCCACAGAACTTGAAGATGAGTGGTGGGGA 1032
 QY 1016 ACTGTGAGACAGGTGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1075
 Db 1033 ACCGTGAGACAGGTGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1092
 QY 1076 CCGGTAAAGAGCGCAACCGCTTGTCTTAATGTCAGACGTAATGAGGGAATTTAAG 1135
 Db 1093 CCGGTAAAGAGCGCAACCGCTTGTCTTAATGTCAGACGTAATGAGGGAATTTAAG 1152
 QY 1136 AGACTGCGGTGAACAAACCGGAGAGGTGGGAGCAAGCTCAATGCTATGAGCCCTTAC 1195
 Db 1153 AGACTGCGGTGAACAAACCGGAGAGGTGGGAGCAAGCTCAATGCTATGAGCCCTTAC 1212
 QY 1196 GAGTGGGCTTACACCGGTGCTAATGAGGCTGATACAGAGGCTGCAAGCTAGAGTATG 1255
 Db 1213 GAGTGGGCTTACACCGGTGCTAATGAGGCTGATACAGAGGCTGCAAGCTAGAGTATG 1272
 QY 1256 AGCGAATCCCAAAAGTACGTGATGTCGGATGGAATGGAATGGAATGGAATGGAATGGAAT 1315
 Db 1273 AGCGAATCCCAAAAGTACGTGATGTCGGATGGAATGGAATGGAATGGAATGGAATGGAAT 1332
 QY 1316 TCGGAATGCTAGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 1374
 Db 1333 TCGGAATGCTAGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 1392
 QY 1375 ACACACCGCCGCTCACACATGAGGAGTGAATGCTCCAGAGTGAAGCTAGCTTAACCTTC 1434
 Db 1393 ACACACCGCCGCTCACACATGAGGAGTGAATGCTCCAGAGTGAAGCTAGCTTAACCTTC 1452
 QY 1435 GGGGATGGCGGTACACAGAGTGTCAATGACTGGGGT 1473
 Db 1453 GGGG--GGGCGTTCACAGTGTGACCGATGACTGGGGT 1489

RESULT 13
 US-09-967-376-1
 ; Sequence 1, Application US/09967376
 ; Patent No. 6482635
 ; GENERAL INFORMATION:

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,102
FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1

Query Match 69.08; Score 1025.8; DB 4; Length 1830121;
Best Local Similarity 83.3%; Pred. No. 0;
Matches 1228; Conservative 0; Mismatches 237; Indels 10; Gaps 5;

3 TAGCTGATTTGAACGCTGCGGAGGCTTAAACACATGCAAGTGCAGGCGTAAACAGGGG 62
770681 TGGCTCAGATTGAACGCTGCGGAGGCTTAAACACATGCAAGTGCAGGCGTAAACAGGGG 770689
63 AGCTTGC---TCTGCTGACGAGCGGCGGAGTGAATTAACGCGTAAAGAACTTGCCTA 118
770690 AAAGCTTGCCTTCTGCTGACGAGTGGCGGAGCGGAGTGAATTAACGCGTAAAGAACTTGCCTT 770749
119 CTAAGGGGGAACAACATGTTGAAACGCAATGCTTAATACCGCATACCGCTTGAAGGGGGAAG 178
770750 ATGAGGGGGAACAACATGTTGAAACGCAATGCTTAATACCGCATACCGCTTGAAGGGGGAAG 770809
179 GAGGGGACTCTTCGAGCCTTCGCTAATTAGATGAGCCTGCGTGAATTAAGCTTAAGTGT 238
770810 TGGGGG--CTGAGAGGCGGAGTGCATAGGATGAGCCCAAGTGGGATTAAGTGTGT 770867
239 AGGTTAAAGGCTTCCAGAGCGAGCATCTTAATCTGTCTGAGAGATGACCAATGCAAC 298
770868 GGGGTAATGCTTACCAAGCTCGATCTCTAGCTGTCTGAGAGATGACCAAGCAAC 770927
299 TGAGCTGAGACAGCGCCAGACTCTCTACCGGAGGAGCAGAGTGGGGAATTAAGCAATG 358
770928 TGGAATGAGACAGCGTCCAGACTCTCTACCGGAGGAGCAGAGTGGGGAATTAAGCAATG 770987
359 GGGGCAAGCTGATCCAGCATGCCGCTGTGTGAAGAAAGGCTTGAAGTTGAAGCAAC 418
770988 GGGGGAACCTGACGCGCATGCCGCTGTGAAGAAAGGCTTGAAGTTGAAGTTTC 771047
419 TTTCAGGGGTGAGGAAGGTAGATTATAGTTATCATCTTACGCTTACCCAGAA 478
771048 TTTCGATTGAGGAAGGTAGATTATAGTTATCATCTTACGCTTACCCAGAA 771107
479 GAAGCACCAGCTAATCTGTGCGAGAGCCGCGGTAAACAGAGGGTGCAGAGCTTAATC 538
771108 GAAGCACCAGCTAATCTGTGCGAGAGCCGCGGTAAACAGAGGGTGCAGAGCTTAATC 771167
539 GGAATTACTGGGCTTAAAGCGCGTAAAGTGTGTTTGAAGTCGATGGAATTCAGAG 598
771168 GGAATTACTGGGCTTAAAGCGCGTAAAGTGTGTTTGAAGTCGATGGAATTCAGAG 771227
599 GCTCAACCTTGAATGAGCAGCCGATCTGCTAGTAGAGTATGATGAGAGGGGTGGA 658
771228 GCTCAACCTTGAATGAGTATTTGAGCTGGGTAACTAGAGTATTTAGAGAGGGGTGGA 771287
659 TTTCCTGTGAGCGGTAAATGCGTGAATTAAGAAAGAAACATCACTGCGCAAGCGCA 718

771288 TTCACGTGTAGCGGTAAATGCGTGAATGATGAGAGAAATACCGAAGGCGAAGCC 771347
719 CCTTGACTTAATCTGACATCTGAGTGGGAAAGCGTGGGAGCAACAGATTGATACC 778
771348 CCTTGGAATGATGACAGCTGATGGAAGGCGGGGAGCAACAGATTGATACC 771407
779 CTGTAATGTCAGCGCGTAAAGCATGCTTACCTAGCCGTTGGGTTGAATGAATTAGTGGCG 838
771408 CTGTAATGTCAGCGCTTAAAGCATGCTTGAATTTGGGGAATGGGCTTAAGCTGTGCGCG 771467
839 CAGCTAACCAATTAATGATGACCGCTGGGGAGTACCGCGGCAAGCTTAAACTAAATGA 898
771468 TAGCTAACCTGATTAATGATGACCGCTGGGGAGTACCGCGGCAAGCTTAAACTAAATGA 771527
899 ATTGACGGGGCGGCGCACAGAGGGTGAAGCATGTGTTTAATGGAAGCAAGCGAAGAA 958
771528 ATTGACGGGGCGGCGCACAGAGGGTGAAGCATGTGTTTAATGGAAGCAAGCGAAGAA 771587
959 CCTTACCTACTCTTGAATCCACAGACATTTGAAGATGATGTGCTTGGGAACT 1018
771588 CCTTACCTACTCTTGAATCCACAGACATTTGAAGATGATGTGCTTGGGAACT 771647
1019 GTGAGACAGTGTGCTGATGCTGTGCTGAGCTGCTGTTGAATGTTGGTTAAGTCCC 1078
771648 TAGAGACAGTGTGCTGATGCTGTGCTGAGCTGCTGTTGAATGTTGGTTAAGTCCC 771707
1079 GTACAGAGCGCAACCTTGTCTTATTTGCCAGACATGATGTGGGAATTTAAGAGA 1138
771708 GCAAGAGCGCAACCTTATCTTGTGCCAGACAT -TGGTGGGAATCTCAAGAGA 771766
1139 CTGCGGCTACAAACCGAGAAAGTGGGAGCAGATCTTAATCTATGGCCCTTAGAG 1198
771767 CTGCGGCTACAAACCGAGAAAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAG 771826
1199 TAGGGCTACACAGTGTCTAATGCTGATACAGAGGCTCAAGCTAGCTAGTATGAGC 1258
771827 TAGGGCTACACAGTGTCTAATGCTGATACAGAGGCTCAAGCTAGCTAGTATGAGC 771886
1259 GAATCCCAAGATGCTGTGATGCTCGGATTTGAAGTGTGCACTGCACTGCAATGATCG 1318
771887 GAATCCCAAGATGCTGTGATGCTCGGATTTGAAGTGTGCACTGCACTGCAATGATG 771946
1319 GAATCCCAAGATGCTGTGATGCTCGGATTTGAAGTGTGCACTGCACTGCAATGATG 771987
771947 GAATCCCAAGATGCTGTGATGCTCGGATTTGAAGTGTGCACTGCACTGCAATGATG 772006
1379 ACCGCGGTCACACATGAGGATGATGCTTCAAGATGATGATGATGATGATGATGATG 1438
772007 ACCGCGGTCACACATGAGGATGATGCTTCAAGATGATGATGATGATGATGATGATG 772064
1439 ATGCGGTTTACCAAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1473
772065 ATGCGGTTTACCAAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 772099

RESULT 15

US-09-557-884-1/c

Sequence 1, Application US/09557884

Patent No. 6506581

GENERAL INFORMATION:

APPLICANT: Fleischmann et al.

TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome, Fragments

Thereof, and Uses Thereof

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: MD

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 30, 2004, 19:07:51 ; Search time 564.517 Seconds
(without alignments)
9593.704 Million cell updates/sec

Title: US-09-737-297-1

Perfect score: 1486

Sequence: 1 gtagcctcagcttgaacgctc.....ctgggcttgaagctcagcg 1486

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 2434935 seqs, 1822278265 residues

Total number of hits satisfying chosen parameters: 4869878

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

Listing first 45 summaries

Published Applications NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCR_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCRUS_PUBCOMB.seq:*
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- 18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1486	100.0	1486	9	US-09-737-297-1 Sequence 4, Appli
2	1251.8	84.2	1481	9	US-09-737-297-4 Sequence 1, Appli
3	1131	76.1	1501	9	US-09-791-592-1 Sequence 1, Appli
4	1131	76.1	1501	9	US-09-745-476-1 Sequence 1, Appli
5	1131	76.1	1501	9	US-09-821-016-5 Sequence 5, Appli
6	1131	76.1	1501	9	US-09-746-205-1 Sequence 1, Appli
7	1131	76.1	1501	9	US-09-793-920A-1 Sequence 1, Appli
8	1131	76.1	1501	10	US-09-951-720-1 Sequence 1, Appli
9	1131	76.1	1501	11	US-09-791-610-1 Sequence 1, Appli
10	1131	76.1	1501	13	US-10-242-696-1 Sequence 1, Appli
11	1131	76.1	1501	13	US-10-411-319-1 Sequence 1, Appli
12	1131	76.1	1501	15	US-10-218-519-5 Sequence 5, Appli
13	1131	76.1	1501	15	US-10-266-787-5 Sequence 5, Appli
14	1131	76.1	1501	15	US-10-252-518-5 Sequence 5, Appli
15	1131	76.1	1501	15	US-10-105-505-1 Sequence 1, Appli

16	1131	76.1	1501	15	US-10-133-406A-1 Sequence 1, Appli
17	1114.8	75.0	1424	15	US-10-007-527A-12 Sequence 12, Appli
18	1114.8	75.0	1424	15	US-10-007-452-12 Sequence 12, Appli
19	1113	74.9	1506	13	US-10-278-942-1 Sequence 1, Appli
20	1100.2	74.0	1467	9	US-09-726-774-3 Sequence 3, Appli
21	1071	72.1	1467	13	US-10-029-397A-47 Sequence 47, Appli
22	1068	71.9	1487	14	US-10-007-725-5 Sequence 5, Appli
23	1067.2	71.8	1487	9	US-09-726-774-14 Sequence 14, Appli
24	1065.6	71.7	1541	9	US-09-027-439-7 Sequence 7, Appli
25	1065.4	71.7	1500	9	US-09-726-774-4 Sequence 4, Appli
26	1064.6	71.6	1542	11	US-09-940-925A-158 Sequence 158, App
27	1064.6	71.6	1542	11	US-09-941-193A-158 Sequence 158, App
28	1064.6	71.6	1542	15	US-10-061-071-33 Sequence 33, Appli
29	1059.8	71.3	1506	9	US-09-027-439-3 Sequence 3, Appli
30	1054.4	71.0	1429	10	US-09-934-868-81 Sequence 81, Appli
31	1053.6	70.9	1549	9	US-09-912-020-89 Sequence 89, Appli
32	1053.6	70.9	1549	9	US-09-912-020-242 Sequence 242, App
33	1053.6	70.9	1549	9	US-09-912-020-402 Sequence 402, App
34	1051.4	70.8	1537	13	US-10-029-397A-46 Sequence 46, Appli
35	1051.2	70.7	1485	13	US-10-029-397A-48 Sequence 48, Appli
36	1051.2	70.7	1541	9	US-09-726-774-2 Sequence 2, Appli
37	1049.4	70.6	1505	9	US-09-027-439-4 Sequence 4, Appli
38	1046	70.4	1534	13	US-10-029-397A-35 Sequence 35, Appli
39	1042.6	70.2	1505	9	US-09-027-439-6 Sequence 6, Appli
40	1034	69.6	1450	9	US-09-726-774-1 Sequence 1, Appli
41	1032.8	69.5	1532	14	US-10-007-725-6 Sequence 6, Appli
42	1029	69.2	105184	11	US-09-847-513A-1 Sequence 1, Appli
43	1028.2	69.2	1540	10	US-09-967-375-1 Sequence 1, Appli
44	1028.2	69.2	1540	15	US-10-260-647-1 Sequence 1, Appli
45	1025.8	69.0	1547	12	US-10-418-861B-53 Sequence 53, Appli

ALIGNMENTS

RESULT 1
US-09-737-297-1
Sequence 1, Application US/09737297
Patent No. US20020072108A1
GENERAL INFORMATION:
APPLICANT: Berry, Mark
APPLICANT: Griffiths, Allen
APPLICANT: Hill, Philip
APPLICANT: Laybourne-Parry, Johanna
TITLE OF INVENTION: Processes and Organisms for the Production of Antifreeze Protein
FILE REFERENCE: F3247
CURRENT APPLICATION NUMBER: US/09/737,297
CURRENT FILING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: GB 9929696.4
PRIOR FILING DATE: 1999-12-15
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 1486
TYPE: DNA
ORGANISM: Marinomonas protea
US-09-737-297-1

Query Match 100.0%; Score 1486; DB 9; Length 1486;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGCTCAATGAAAGCGGCGAGGCTTAACATGCAAGTCGACGGTAACAG 60
DB 1 GTTAGCTCAATGAAAGCGGCGAGGCTTAACATGCAAGTCGACGGTAACAG 60
QY 61 GGAAGCTTCTCTGCTGACGAGCGGCGAGGCTGAGTAACGGGTAGTAATGCTACT 120
DB 61 GGAAGCTTCTCTGCTGACGAGCGGCGAGGCTGAGTAACGGGTAGTAATGCTACT 120
QY 121 AGAGGGGAGCAACATGTGGAAAGCATGCTAATACCGCATAGCCCTGAGGGGAAAGA 180
DB 121 AGAGGGGAGCAACATGTGGAAAGCATGCTAATACCGCATAGCCCTGAGGGGAAAGA 180

Db 121 AGAGGGGACACATGTGAAAAGCATGCTAATACCCATACGCCCTTAGGGGAAAAGCA 180
Qy 181 GGGGAGCTCTTCGAGAGCTTCGCTATTAGATAGAGCTCGTGAATTAGTTAGTTGATG 240
Db 181 GGGGAGCTCTTCGAGAGCTTCGCTATTAGATAGAGCTCGTGAATTAGTTAGTTGATG 240
Qy 241 GGTAAAGGCTTACCAAGGCGAGATCTCTAATCTGATGAGGAGTGAACAGTACACTG 300
Db 241 GGTAAAGGCTTACCAAGGCGAGATCTCTAATCTGATGAGGAGTGAACAGTACACTG 300
Qy 301 GGAATGAGACAGGCCCAAGCTCTCAAGGAGGACAGATGGGGAATATTGACAAATGGG 360
Db 301 GGAATGAGACAGGCCCAAGCTCTCAAGGAGGACAGATGGGGAATATTGACAAATGGG 360
Qy 361 CGCAAGCTTATCCAGCTATGCCGCTGTGTGAAGAAGGCTTAGGCTTGTAAAGCACTT 420
Db 361 CGCAAGCTTATCCAGCTATGCCGCTGTGTGAAGAAGGCTTAGGCTTGTAAAGCACTT 420
Qy 421 TCAGGGGTGAGAAAGGATGATAGTTAATACGTTATCACTTGAAGCTTAGCCCAAGA 480
Db 421 TCAGGGGTGAGAAAGGATGATAGTTAATACGTTATCACTTGAAGCTTAGCCCAAGA 480
Qy 481 AGCAGCGGCTAATCTGTGTGACAGACCGCGGTAAATACAGAGGCTGCAAGCTTAATCG 540
Db 481 AGCAGCGGCTAATCTGTGTGACAGACCGCGGTAAATACAGAGGCTGCAAGCTTAATCG 540
Qy 541 AATTAAGGCGGTAAAGCGCGGTAGTGTGTTAATGAGTGAATGCAATCCAGAGGC 600
Db 541 AATTAAGGCGGTAAAGCGCGGTAGTGTGTTAATGAGTGAATGCAATCCAGAGGC 600
Qy 601 TCAACCTTGAATGAGCAACCGGATACGCTAGCTAGATAGATGATGATGAGAGGCTG 660
Db 601 TCAACCTTGAATGAGCAACCGGATACGCTAGCTAGATAGATGATGATGAGAGGCTG 660
Qy 661 TCCGTGTAGCGGTGAAATGCGGTAGATATGAGAAAGCAATAGAGGCGAGGCGACCC 720
Db 661 TCCGTGTAGCGGTGAAATGCGGTAGATATGAGAAAGCAATAGAGGCGAGGCGACCC 720
Qy 721 CTGAGCTAATATGACATGAGGTGCGAAAGCGTGGGAGCAACAGATTAATGATACCT 780
Db 721 CTGAGCTAATATGACATGAGGTGCGAAAGCGTGGGAGCAACAGATTAATGATACCT 780
Qy 781 GGTGTGACAGCGGTAAAGCATGCTAATAGCGCTTGGGTTTATGATGATGATGATG 840
Db 781 GGTGTGACAGCGGTAAAGCATGCTAATAGCGCTTGGGTTTATGATGATGATGATG 840
Qy 841 GCTAACGCAATTAAGTAGACGCTGGGAGTACGCGCGCAAGGTTAAATCAATGAT 900
Db 841 GCTAACGCAATTAAGTAGACGCTGGGAGTACGCGCGCAAGGTTAAATCAATGAT 900
Qy 901 TGAAGGCGGCGCGCAAGCGGTGAGCATGTGTGTTAATGGAAGCAACGGAAGACC 960
Db 901 TGAAGGCGGCGCGCAAGCGGTGAGCATGTGTGTTAATGGAAGCAACGGAAGACC 960
Qy 961 TTACCTAATCTGATCAACAGAACTTTGAGAGATCAGATGATGATGATGATGATG 1020
Db 961 TTACCTAATCTGATCAACAGAACTTTGAGAGATCAGATGATGATGATGATGATG 1020
Qy 1021 GAGAAGGCTGCTGATGCTGTGTGCTAGCTGTGTTGTAATGTTGGTTAAGTCCGT 1080
Db 1021 GAGAAGGCTGCTGATGCTGTGTGCTAGCTGTGTTGTAATGTTGGTTAAGTCCGT 1080
Qy 1081 AAGAGGCGCAACCTTGTCTTATTTTSCAGACGTAATGATGATGATGATGATGATG 1140
Db 1081 AAGAGGCGCAACCTTGTCTTATTTTSCAGACGTAATGATGATGATGATGATGATG 1140
Qy 1141 GCCGGTGAACAAACCGGAGAAAGGTGGGAGCAGCTCAATGATGATGATGATGATG 1200
Db 1141 GCCGGTGAACAAACCGGAGAAAGGTGGGAGCAGCTCAATGATGATGATGATGATG 1200
Qy 1201 GGGGTACACAGCTCTCAATGAGGTATACAGAGGCTGCAAGCTTACCAATGATGATG 1260
Db 1201 GGGGTACACAGCTCTCAATGAGGTATACAGAGGCTGCAAGCTTACCAATGATGATG 1260

Qy 1261 ATCCCAACAAAGTACGCTGATGCTGAGTGGAGTGTGCAATGCACTTCAATGAACTGGA 1320
Db 1261 ATCCCAACAAAGTACGCTGATGCTGAGTGGAGTGTGCAATGCACTTCAATGAACTGGA 1320
Qy 1321 ATCCGCTAGTAATGAGTACGAAATGTCACGAGTGAATACGTTCCCGGAGCTTGTACAC 1380
Db 1321 ATCCGCTAGTAATGAGTACGAAATGTCACGAGTGAATACGTTCCCGGAGCTTGTACAC 1380
Qy 1381 CGCCGCTACACACATGAGGAGTGTGATGCTCCAGAAAGTACGTTAACCTTCCGGGAT 1440
Db 1381 CGCCGCTACACACATGAGGAGTGTGATGCTCCAGAAAGTACGTTAACCTTCCGGGAT 1440
Qy 1441 GGGGTTACCAAGGAGTGTGATGCTGAGTGGGTTGAAGTCTACGCG 1486
Db 1441 GGGGTTACCAAGGAGTGTGATGCTGAGTGGGTTGAAGTCTACGCG 1486

RESULT 2
US-09-737-297-4
; Sequence 4: Application US/09737297
; Patent No. US20020072108A1
; GENERAL INFORMATION:
; APPLICANT: Bery, Mark
; APPLICANT: Griffiths, Allen
; APPLICANT: Hill, Philip
; APPLICANT: Laybourne-Parry, Johanna
; APPLICANT: Mills, Sarah
; TITLE OF INVENTION: Processes and Organisms for the Production of Antifreeze Prote
; FILE REFERENCE: F3247
; CURRENT APPLICATION NUMBER: US/09/737,297
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: GB 9929696.4
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 1481
; TYPE: DNA
; ORGANISM: Marinomonas communis
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: (1)..(1)
; OTHER INFORMATION: base identity unsure
; NAME/KEY: Unsure
; LOCATION: (203)..(204)
; OTHER INFORMATION: base identity unsure
; NAME/KEY: Unsure
; LOCATION: (840)..(840)
; OTHER INFORMATION: base identity unsure
; NAME/KEY: Unsure
; LOCATION: (964)..(965)
; OTHER INFORMATION: base identity unsure
; NAME/KEY: Unsure
; LOCATION: (1142)..(1142)
; OTHER INFORMATION: base identity unsure
; NAME/KEY: Unsure
; LOCATION: (1182)..(1182)
; OTHER INFORMATION: base identity unsure
; NAME/KEY: Unsure
; LOCATION: (1185)..(1186)
; OTHER INFORMATION: base identity unsure
; NAME/KEY: Unsure
; LOCATION: (1449)..(1449)
; OTHER INFORMATION: base identity unsure
US-09-737-297-4

Query Match 84.2%; Score 151.8; DB 9; Length 1481;
Best Local Similarity 93.7%; Pred. No. 0;
Matches 1374; Conservative 1; Mismatches 83; Indels 9; Gaps 7;
3 TAGCTCAGATTGAAGCTTGGCGGCGGCTTAAACATGCAAGTGAAGGCGTAAACAGGGG 62

Db 21 TGGCTCAGATTGAACGCTGCGGAGGCTT-AACACATGCAATGACGCTAACATTCG 79
QY 63 -AGCTTGTCTCCT-GCTGACGAGCGGCGGACGGGTGATTAACGGCTAGGAATTCGCTAGT 120
Db 80 TAGCTGTGTAAGATGACGAGCGGCGGACGGGTGATTAACGGCTAGGAATTCGCTAGT 139
QY 121 AGAGGGGAGCAACATGTGTAAGCAATGCTTAATACCGCATACGCTCGAGGGGAGAAAGG 180
Db 140 AGTGGGGAGCAACATGTGTAAGCAATGCTTAATACCGCATACGCTCGAGGGGAGAAAGG 199
QY 181 GGGGACTCTTCGAGGACCTTCGCTTAATGATGAGCTGCGTGAATTAAGTATGCTAGT 240
Db 200 GGG--NNTCTTCGAGCTTCCTGCTTAATGATGAGCTGCGTGAATTAAGTATGCTAGT 257
QY 241 GGTAAAGGCTTACCAAGGCGACGATCTGTAATCTGATGAGAGGATGACCAAGTCACTG 300
Db 258 GGTAAAGGCTTACCAAGGCGACGATCTGATGCTGATGAGAGGATGATGACCAAGTCACTG 317
QY 301 GGAAGTGAACACGAGCGCCAGACTCTTAACGGAGGAGCAGATGGGGAAATATTGAACATGG 360
Db 318 GGAAGTGAACACGAGCGCCAGACTCTTAACGGAGGAGCAGATGGGGAAATATTGAACATGG 377
QY 361 GCGAAGCTGATCCAGCGCATGCGCGTGTGTAAGAGGCGCTTGGGTGTAAGAGACTT 420
Db 378 GCGAAGCTGATCCAGCGCATGCGCGTGTGTAAGAGGCGCTTGGGTGTAAGAGACTT 437
QY 421 TCAGGGGTGAGAGAGGATGATAGTTAATACGTTATCATCTTGAAGTCCAGAGAG 480
Db 438 TCAGAGGTGAGAGAGGATGATAGTTAATACGTTATCATCTTGAAGTCCAGAGAG 497
QY 481 AGCACCCTGTAATCTGTGTCAGACAGCGCGCTTAATACAGAGGATGCAAGCTTAATCG 540
Db 498 AGCACCCTGTAATCTGTGTCAGACAGCGCGCTTAATACAGAGGATGCAAGCTTAATCG 557
QY 541 AATTACTGGCGCTAAAGCGCGGTGATGTTGTTAATGATGATGATGATGATGATGATGATG 600
Db 558 AATTACTGGCGCTAAAGCGCGGTGATGTTGTTAATGATGATGATGATGATGATGATGATG 617
QY 601 TCAACCTTGGAAATGCAACCCGATGCTGCTAGTGAATGATGATGATGATGATGATGATG 660
Db 618 TCAACCTTGGAAATGCAACCCGATGCTGCTAGTGAATGATGATGATGATGATGATGATG 677
QY 661 TCCTGTGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
Db 678 TCCTGTGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 737
QY 721 CTGGAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
Db 738 CTGGAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 797
QY 781 GGTAGTCCACCGCGTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 839
Db 798 GGTAGTCCACCGCGTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 857
QY 840 AGCTTAACGCAATAGTGAACCGCTGGGAGATGAGCGCGCAAGGTTAAATCTCAATGAA 899
Db 858 AGCTTAACGCAATAGTGAACCGCTGGGAGATGAGCGCGCAAGGTTAAATCTCAATGAA 917
QY 900 TTGACGGGGCGCCGCAAGCGGTGAGCAATGATTAATTCAGAGCAACGCGCAAGAAC 959
Db 918 TTGACGGGGCGCCGCAAGCGGTGAGCAATGATTAATTCAGAGCAACGCGCAAGAAC 977
QY 960 CTTAACCTTCTTGAATCAGACAGAACTTTAGAGATCAGATGATGATGATGATGATGATG 1019
Db 978 CTTAACCTTCTTGAATCAGACAGAACTTTAGAGATGATGATGATGATGATGATGATG 1037
QY 1020 TGAAGACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1079
Db 1038 TGAAGACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1097
QY 1080 TAAACGAGCAACCGCTGCTTATTTGACAGCAATGATGATGATGATGATGATGATGATG 1139
Db 1098 TAAACGAGCAACCGCTTATTTGACAGCAATGATGATGATGATGATGATGATGATGATG 1156

QY 1140 TGGCGGTGACAAACCGGAGAGAGTGGGAGCAGCTCAAGTCAATGATGAGCCCTTACAGAT 1199
Db 1157 TGGCGGTGACAAACCGGAGAGAGTGGGAGCAGCTCAAGTCAATGATGAGCCCTTACAGAT 1216
QY 1200 AGGGCTACACAGCTGTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 1259
Db 1217 AGGGCTACACAGCTGTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 1276
QY 1260 AATCCCAAAAGTACGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1319
Db 1277 AATCCCAAAAGTACGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1336
QY 1320 AATCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1379
Db 1337 AATCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1396
QY 1380 CCGCCCGTACACAGCTGTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 1439
Db 1397 CCGCCCGTACACAGCTGTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 1454
QY 1440 TGGCGGTACACAGCTGTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 1466
Db 1455 TGGCGGTACACAGCTGTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 1481

RESULT 3
US-09-791-592-1
; Sequence 1, Application US/09791592
; Patent No. US20010021223A1
; GENERAL INFORMATION:
; APPLICANT: Canon Inc.
; TITLE OF INVENTION: Polyhydroxyalkanoate containing 3-hydroxybenzoalkanoic acid ;
; FILE REFERENCE: 4396021
; CURRENT APPLICATION NUMBER: US/09/791,592
; CURRENT FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 1
; SEQ ID NO 1
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii 161 strain.
US-09-791-592-1

Query Match 76.1%; Score 1131; DB 9; Length 1501;
Best Local Similarity 88.2%; Pred. No. 1e-298; Indels 9; Gaps 6;
Matches 1299; Conservative 0; Mismatches 165;

Db 13 TGAACGCTGGCGGAGGCTTAAACATGCAATGCAAGTGCAGCGTAAACAGGGAGCTTCTCC 72
1 TGAACGCTGGCGGAGGCTTAAACATGCAATGCAAGTGCAGCGG -ATGACGGGAGCTTCTCC 58
QY 73 TGTGACGAGAGCGGACCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 132
Db 59 TGAATTC-AGGAGGAGAGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 117
QY 133 CATGGAAGAGCATGCTTAATACCGCATACGCTGAGGGGAGAGGAGGAGGAGGAGGAGGAGG 192
Db 118 CGTCTGGAAGAGCATGCTTAATACCGCATACGCTGAGGGAGAGGAGGAGGAGGAGGAGGAGG -CCTTC 175
QY 193 GAGCCTTCGCTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 252
Db 176 GGGCGCTTCGCTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 235
QY 253 CCAAGGAGAGATGCTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 312
Db 236 CCAAGGAGAGATGCTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 295
QY 313 GGGCCAGACTCTTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 372
Db 236 GGTTCAGACTCTTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 355
QY 373 CCAAGCAGTCCGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 432

DB 356 CCAGCCATGCCCGCTGTGAAAGAGCTTTCGGATGTGTAAGCACTTAAAGTGGGAGG 415
QY 433 AAGGTGATAGTTAATACGTTATCATCTTGAAGTACCCGAGAGAGCAAGCCGCTAA 492
DB 416 AAGGGATTAACCTAATACGTTAGTGTGCTTTGACGTTACGACAGATTAAGACCGGCTAA 475
QY 493 CTCTGTGACAGAGCCGCGGTATTCAGAGGGGTGAAGCGTTAATCCGAATTAATGAGGCG 552
DB 476 CTCTGTGACAGAGCCGCGGTATTCAGAGGGGTGAAGCGTTAATCCGAATTAATGAGGCG 535
QY 553 TAAAGCGCGGTAGTGTGTTGTAAAGTGAATGTAATCCAGGGCTCAACCTTGA 612
DB 536 TAAAGCGCGGTAGTGTGTTGTAAAGTGAATGTAATCCAGGGCTCAACCTTGA 595
QY 613 TGGCACCAGATATGCTAGTACGATAGTGAAGGGGTGGAATTTCTGTGTGCG 672
DB 596 CTGCATTCAAAATGTCMAAGCTAGATGTAGAGGGGTGGAATTTCTGTGTGCG 655
QY 673 GTGAATGCGTAGATATAGAAAGAAACATCAATGCGAGGAGCAACCTGACTAATAC 732
DB 656 GTGAATGCGTAGATATAGAAAGAAACATCAATGCGAGGAGCAACCTGACTAATAC 715
QY 733 TGACACTGAGGTGCGAAAGCGTGGGAGCAACAGGATTAATACCTGTGATGCC 792
DB 716 TGACACTGAGGTGCGAAAGCGTGGGAGCAACAGGATTAATACCTGTGATGCC 775
QY 793 CGTAAAGATGTCTAGTACCGCTGG - GTGTAAATGACTTATGAGGCGAGCTAAGCAA 850
DB 776 CGTAAAGATGTCTAGTACCGCTGGAGCGCTTGAAGCTTATGAGGCGAGCTAAGCAA 835
QY 851 TAAGTAGACCGCTGGGAGGATACGCGCGCAAGGTTAAACTCAATGAATGACGGGCG 910
DB 836 TAAGTAGACCGCTGGGAGGATACGCGCGCAAGGTTAAACTCAATGAATGACGGGCG 895
QY 911 CCGCACAAGCGGTGAGCATGTGTATTTGAAGCAACGCGAAGACCTTACTACTC 970
DB 896 CCGCACAAGCGGTGAGCATGTGTATTTGAAGCAACGCGAAGACCTTACTACTC 955
QY 971 TTGACATCCACAGACATTTGAGAGATGATGTGCTTCGGGAATCTGTAGACAGGTG 1030
DB 956 TTGACATCCACAGACATTTGAGAGATGATGTGCTTCGGGAATCTGTAGACAGGTG 1015
QY 1031 CTGCATGCGCTGTCTAGCTGTGTGTGAATGTTGGGTAAAGTCCGCTAAGAGGCA 1090
DB 1016 CTGCATGCGCTGTCTAGCTGTGTGTGAATGTTGGGTAAAGTCCGCTAAGAGGCA 1075
QY 1091 ACCCTGTCTTATTGGCAGACGTAATGTGGGAATTAAAGAGACTCCGCTGACA 1150
DB 1076 ACCCTGTCTTATTGGCAGACGTAATGTGGGAATTAAAGAGACTCCGCTGACA 1135
QY 1151 AACCGAGAGAGGTGGGAGACAGCTCAAGTCAATGAGCCCTTAAGAGTGGGCTAC 1210
DB 1136 AACCGAGAGAGGTGGGAGATGACGTCAAGTCAATGAGCCCTTAAGAGTGGGCTAC 1195
QY 1211 CGTGTCAATGAGCGATACAGAGGGCTCAAGCTAAGCATAGTAGAGCAATCCCAAA 1270
DB 1196 CGTGTCAATGAGCGATACAGAGGGTTCAGAGCCGAGGTGAAGCTAATCCCAAA 1255
QY 1271 GTAAGTGTAGTCCGATTTGAGACTGTCAACTGCACTCCATGAAGTCCGAATCCGTA 1330
DB 1256 ACGATGTAGTCCGATTCGCACTGTCAACTGCACTCCGATGAATCCGTAAGTA 1315
QY 1331 ATGCGATACAGATGTCCGAGATAGCTTCCGGGGCTGTGTACACACCGCCGTAC 1390
DB 1316 ATGCGATACAGATGTCCGAGATAGCTTCCGGGGCTGTGTACACACCGCCGTAC 1375
QY 1391 ACCATGAGAGTGTATGCTTCCAGAGTACTAAGCTTACCTTCGGGAGTGGCGTTAC 1450
DB 1376 ACCATGAGAGTGTATGCTTCCAGAGTACTAAGCTTACCTTCGGGAGTGGCGTTAC 1433
QY 1451 ACGAGTGTCAATGACTGGGCTTGAAGCTTAC 1483

DB 1434 ACGTGTATTCATGACTGGGGTGAAGTCGAC 1466
RESULT 4
US-09-745-476-1
Sequence 1, Application US/09745476
Patent No. US20010029039A1
GENERAL INFORMATION:
APPLICANT: CANON INC.
TITLE OF INVENTION: Preparation of Poly-hydroxylalkanoic Acid
FILE REFERENCE: 435108
CURRENT APPLICATION NUMBER: US/09/745,476
CURRENT FILING DATE: 2000-12-26
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Microsoft Word
SEQ ID NO. 1
LENGTH: 1501
TYPE: DNA
ORGANISM: Pseudomonas jessenii P161 ; FERM P-17445
US-09-745-476-1
Query Match 76.1%; Score 1131; DB 9; Length 1501;
Best Local Similarity 88.2%; Pred. No. 1e-298;
Matches 1299; Conservative 0; Mismatches 165; Indels 9; Gaps 6;
QY 13 TGAAGCTGGCGGAGGCTTAAACATGCAAGTGAAGCGGTACAGGGAGCTTGCTCC 72
DB 1 TGAAGCTGGCGGAGGCTTAAACATGCAAGTGAAGCGGTACAGGGAGCTTGCTCC 58
QY 73 TGCATACAGGCGGCGAGAGGCTGATACAGGCTGATGATGCTGATAGAGGGAGCAA 132
DB 59 TGAATTC-AGCGCGGAGAGGCTGATGATGCTGATGATGCTGATAGAGGGAGCAA 117
QY 133 CATGTGAAAGCATGTCTAATACGACATACGCGCTGAGGGGAAAGAGGAGGACTTTCG 192
DB 118 GCTTCGAAGGAGAGGCTAATACCGCATACGCTCTACGGAAGAAAGAGGAGG- -CCTTC 175
QY 193 GAGCTTCCGCTATTAATGATGAGCTGCTGATGATTAATGCTAGTAAAGGCTA 252
DB 176 GGGCTTCCGCTATGATGATGAGCTGATGATGATGATGATGATGATGATGATGATG 235
QY 253 CCAAGGCAAGATCTCTAATGCTGTGAGAGATGACAGTCACTGAGGAGTGAACAC 312
DB 236 CCAAGGCAAGATCTCTAATGCTGTGAGAGATGACAGTCACTGAGGAGTGAACAC 295
QY 313 GCGCCAGATCTCTACGAGGAGCAAGATGAGGAAATTTGACAAATGAGGCGCAAGCTGAT 372
DB 296 GGTTCAGATCTCTACGAGGAGCAAGATGAGGAAATTTGACAAATGAGGCGCAAGCTGAT 355
QY 373 CCAAGCAGTCCGCTGTGTGAAGAGGCTTAAAGGCTTAAAGGCTTAAAGGCTTAAAGG 432
DB 356 CCAAGCAGTCCGCTGTGTGAAGAGGCTTAAAGGCTTAAAGGCTTAAAGGCTTAAAGG 415
QY 433 AAGGTGATAGTTAATGCTTATCATCTTGAAGTACCTTGAAGTACCTTGAAGTACCT 492
DB 416 AAGGCAATTAACCTAATACGTTAGTGTGCTTTGACGTTACGACAGATTAAGACCGGCTAA 475
QY 493 CTCTGTGACAGAGCCGCGGTATTCAGAGGGGTGAAGCGTTAATCCGAATTAATGAGGCG 552
DB 476 CTCTGTGACAGAGCCGCGGTATTCAGAGGGGTGAAGCGTTAATCCGAATTAATGAGGCG 535
QY 553 TAAAGCGCGGTAGTGTGTTGTAAAGTGAATGTAATCCAGGGCTCAACCTTGA 612
DB 536 TAAAGCGCGGTAGTGTGTTGTAAAGTGAATGTAATCCAGGGCTCAACCTTGA 595
QY 613 TGGCACCAGATATGCTAGTACGATAGTGAAGGGGTGGAATTTCTGTGTGCG 672
DB 596 CTGCATTCAAAATGTCMAAGCTAGATGTAGAGGGGTGGAATTTCTGTGTGCG 655
QY 673 GTGAATGCGTAGATATAGAAAGAAACATCAATGCGAGGAGCAACCTGACTAATAC 732
DB 656 GTGAATGCGTAGATATAGAAAGAAACATCAATGCGAGGAGCAACCTGACTAATAC 715

Db 1016 CTGATGCTGTCGTACAGTCTGTCGTGAGATGTTGGGTAAAGTCCCGTAACGACGCA 1075
Qy 1091 ACCCTTGTCTTATTTGCCGACGCTAATGCTGGGAACCTTAAGGAGACTGCCGTGACA 1150
Db 1076 ACCCTTGTCTTATTTGCCGACGCTAATGCTGGGAACCTTAAGGAGACTGCCGTGACA 1135
Qy 1151 AACCGAGAGAGGTGGGAGACGACGTCATGATGAGCCCTTACGAGTAAAGGCTACACA 1210
Db 1136 AACCGAGAGAGGTGGGAGACGACGTCATGATGAGCCCTTACGAGTAAAGGCTACACA 1195
Qy 1211 CGTGTCAATGCGGTATACAGAGGCTGACAGCCGCGAGGTGAGCTTAATCCACAAA 1270
Db 1196 CGTGTCAATGCGGTATACAGAGGCTGACAGCCGCGAGGTGAGCTTAATCCACAAA 1255
Qy 1271 GTACGTGCTGTCGCGATGAGTGTGACACTGACCTCCATGAGTGGAAATCGGTAGTA 1330
Db 1256 ACCGATCGTAGTCCGATCCGATCGCACTGCACTGCTGAAAGTCCGAAATCGGTAGTA 1315
Qy 1331 ATCGTAATCAGAAATGTCACGCTGAAATACGTTCCGCGGCTTGTACACACCGCCGTAC 1390
Db 1316 ATCGGATCAGAAATGTCACGCTGAAATACGTTCCGCGGCTTGTACACACCGCCGTAC 1375
Qy 1391 ACCATGGAGTGTATGCTCCAGAGTACGTAAGCTTAACCTTCGGGAGTGGCGTTAC 1450
Db 1376 ACCATGGAGTGTGACACAGAGTACGTAAGCTTAACCTTCGGGAGTGGCGTTAC 1433
Qy 1451 ACGGAGTGTCAATGACTGCGGCTTGAAGTCTAC 1483
Db 1434 ACGGAGTGTCAATGACTGCGGCTTGAAGTCTAC 1466

RESULT 6

US-09-748-205-1
; Sequence 1, Application US/09748205
; Patent No. US2002022253A1
; GENERAL INFORMATION:
; APPLICANT: Canon, Inc.
; TITLE OF INVENTION: Polyhydroxyalkanoate, its manufacturing method, and microorganism
; FILE OF INVENTION: those are used for the method.
; FILE REFERENCE: 4351009
; CURRENT APPLICATION NUMBER: US/09/748,205
; CURRENT FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 1
; SEQ ID NO: 1
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii 161 strain.
US-09-748-205-1

Query Match 76.1%; Score 1131; DB 9; Length 1501;
Best local similarity 88.2%; Pred. No. 1e-298;
Matches 1299; Conservative 0; Mismatches 165; Indels 9; Gaps 6;
Qy 13 TGAACGCTGGCGGCGGCTTAAACATGCAAGTCGACGCTPAACAGGGGAGCTTGTCC 72
Db 1 TGAACGCTGGCGGCGGAGCCT-AAACATGCAAGTCGACGCG-ATGACGGGAGCTTGTCC 58
Qy 73 TGTGAGAGAGCGGCGGAGCGGCTGAGTAACGCGTGAATCTGCTAGTAGAGGGGACAA 132
Db 59 TGAATTC-AGCGGCGGAGCGGCTGAGTAATGCTGAGTAATCTGCTGTAATGAGGACAA 117
Qy 133 CATGTGAAAACGATGCTAATACCGCATACGCCCTGAGGGGAAAAGAGGGGACTTTCG 192
Db 118 GGTCTGAAAAGGAGCGCTAATACCGCATACGCTCTACGGGAAAAGCAGGGGA--CCTTC 175
Qy 193 GAGCTTCGGCTATAGTAGAGCTGCGTGAAGTTGCTAGTGTGAGGTAAAGGCTA 252
Db 176 GGGCTTCGCTCTCAATAGAGCTGAGTGTGCTAGTGTGAGGTAAAGGCTA 235
Qy 253 CCAAGGCGAGATCTCTAATGCTGAGAGATGACAGTCAACTGGGACTGAGACAC 312
Db 236 CCAAGGCGAGATCTCTAATGCTGAGAGATGATCACTCACTGGAATGAGACAC 295

Qy 313 GGCACGACTCTCTACGAGGAGCAGAGTGGGAAATATGACAAATGGGCGCAACTGAT 372
Db 296 GGTCCGACTCTCTACGAGGAGCAGAGTGGGAAATATGACAAATGGGCGCAACTGAT 355
Qy 373 CCAAGCAGTCCGCGTGTGTAAAGAGCCTTAAGGTGTAAAGACTTTCAGGGGTAGG 432
Db 356 CCAAGCAGTCCGCGTGTGTAAAGAGCCTTCCGATGTAAAGACTTTCAGGGGTAGG 415
Qy 433 AAGGGGATAGGTAAATGCTATCATCTTACAGTGGCCCGCAAGAGACCGGGTAA 492
Db 416 AAGGGGATTAACCTTAATAGCTTATGCTTTTACGTTACCGACAAATAGACCGGGTAA 475
Qy 493 CTCTGTCCAGAGCCGCGTAAATACAGAGGTCAACCGTTAATCGAATTAAGGCG 552
Db 476 CTCTGTCCAGAGCCGCGTAAATACAGAGGTCAACCGTTAATCGAATTAAGGCG 535
Qy 553 TAAAGGCGCGTGTGTGTGTAAAGTGTGAAATCCGAGGCTCAACTTGGAA 612
Db 536 TAAAGGCGCGTGTGTGTGTAAAGTGTGAAATCCGAGGCTCAACTTGGAA 595
Qy 613 TGGACCCGATCTGCTAGCTAGATGTGTAGAGGGGTGGAATTTCTGTGTAGCG 672
Db 596 CTGCAATCAAACTGACAAAGTATGATGATGAGGTGTGGAATTTCTGTGTAGCG 655
Qy 673 GTGAAATGCTGATATAGAAAGAACTCATGTGCGAAGCGCACCTTGAATATC 732
Db 656 GTGAAATGCTGATATAGAAAGAACTCATGTGCGAAGCGCACCTTGAATATC 715
Qy 733 TGCACCTGAGTGCAGAAAGCGGGGAGCAACAGAAATTAATACCTGTAGTCCAGC 792
Db 716 TGCACCTGAGTGCAGAAAGCGGGGAGCAACAGAAATTAATACCTGTAGTCCAGC 775
Qy 793 CGTAAACGATGTCTAATAGCCGTGG--GTTGTAATGACTTAATGTGGCGCACTAACCA 850
Db 776 CGTAAACGATGTCTAATAGCCGTGGAGCTTGAAGCTTAATGTGGCGCACTAACCA 835
Qy 851 TAAGTGAACCGGCTGGGAGTAACGCGCGCAAGTTAAATCAATGATTAAGAGGGGCG 910
Db 836 TAAGTGAACCGGCTGGGAGTAACGCGCGCAAGTTAAATCAATGATTAAGAGGGGCG 895
Qy 911 CCGCACAGCGGTGAGCATGTGTTTATTCAGAGCAACGGAAGAACTTACTCTC 970
Db 896 CCGCACAGCGGTGAGCATGTGTTTATTCAGAGCAACGGAAGAACTTACTCTC 955
Qy 971 TTGACATCCACAGAACTTTGAGAGTCAATGTGCTTGGGAACTGAGACAGGTG 1030
Db 956 TTGACATCCATGAACCTTTCAGAGATGATGGGTCTTGGGAACTGAGACAGGTG 1015
Qy 1031 CTGATGCTGTCTGACGCTGCTGTGTAATGTGGTTAGTCCGTAACGAGCGCA 1090
Db 1016 CTGATGCTGTCTGACGCTGCTGTGTAATGTGGTTAGTCCGTAACGAGCGCA 1075
Qy 1091 ACCCTGTCTTATTTGCCGACGCTAATGCTGGGAACCTTAAGGAGACTGCCGTGACA 1150
Db 1076 ACCCTGTCTTATTTGCCGACGCTAATGCTGGGAACCTTAAGGAGACTGCCGTGACA 1135
Qy 1151 AACCGAGAGAGGTGGGAGACGACGTCATGATGAGCCCTTACGAGTAAAGGCTACACA 1210
Db 1136 AACCGAGAGAGGTGGGAGACGACGTCATGATGAGCCCTTACGAGTAAAGGCTACACA 1195
Qy 1211 CGTGTCAATGCGGTATACAGAGGCTGACAGCCGCGAGGTGAGCTTAATCCACAAA 1270
Db 1196 CGTGTCAATGCGGTATACAGAGGCTGACAGCCGCGAGGTGAGCTTAATCCACAAA 1255
Qy 1271 GTACGTGCTGTCGCGATGAGTGTGACACTGACCTCCATGAGTGGAAATCGGTAGTA 1330
Db 1256 ACCGATCGTAGTCCGATCCGATCGCACTGCACTGCTGAAAGTCCGAAATCGGTAGTA 1315
Qy 1331 ATCGTAATCAGAAATGTCACGCTGAAATACGTTCCGCGGCTTGTACACACCGCCGTAC 1390
Db 1316 ATCGGATCAGAAATGTCACGCTGAAATACGTTCCGCGGCTTGTACACACCGCCGTAC 1375
Qy 1391 ACCATGGAGTGTGACTGCGGCTTGAAGTCTAC 1483
Db 1434 ACCATGGAGTGTGACTGCGGCTTGAAGTCTAC 1466

PRIOR FILING DATE: 2000-09-14
2000-12-13
2001-05-31
2001-05-31
2001-09-11
NUMBER OF SEQ ID NOS: 1
SEQ ID NO: 1
LENGTH: 1501
TYPE: DNA
ORGANISM: Pseudomonas jessenii 161 strain.
US-09-951-720-1

Query Match 76.1%; Score 1131; DB 10; Length 1501;
Best Local Similarity 88.2%; Pred. No. 1e-298;
Matches 1299; Conservative 0; Mismatches 165; Indels 9; Gaps 6;

QY 13 TGAACGCTGGCGGAGGCTTAAACACATGCAAGTCAAGCGGTAAACAGGGGAGCTTCTCC 72
DB 1 TGAACGCTGGCGGAGGCTTAAACACATGCAAGTCAAGCGGTAAACAGGGGAGCTTCTCC 58
QY 73 TGCTGACGAGCGGCGGAGCGGTGAGTAAACGCTAGAGATCTGCTAGTAGAGGGGAGCA 132
DB 59 TGAATTC-AGCGCGGAGCGGCTGAGTATGCTAGATCTGCTAGTAGAGGGGAGCA 117
QY 133 CATGTGAAACGATGCTAAATACCGCATACGCTTGAAGGGGAGGAGGAGCTTCTG 192
DB 118 CGTCTCGAAAGGAGCGCTAAATACCGCATACGCTTGAAGGGGAGGAGGAGCTTCTG 175
QY 193 GAGCTTCCGCTATTAATAGAGCTGCTGAGATTAAGTATGCTAGTGAAGGTTAAAGGCTTA 252
DB 176 GAGGCTTGGCTATCAATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 235
QY 253 CCAAGCGGAGCGGAGCTTAACTGCTGCTGAGAGATGAACAATGCACTGAGGAGTGAAC 312
DB 236 CCAAGCGGAGCGGAGCTTAACTGCTGCTGAGAGATGAACAATGCACTGAGGAGTGAAC 295
QY 313 GCGCCAGACTCTTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 372
DB 296 GGTCCAGACTCTTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 355
QY 373 CCAGCAGTGCAGGCTGCTGAGAGAGGCTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGG 432
DB 356 CCAGCAGTGCAGGCTGCTGAGAGAGGCTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGG 415
QY 433 AAGGCTGATGAGTAAATGCTTATCATCTTGAAGTGAAGGAGGAGGAGGAGGAGGAGGAG 492
DB 416 AAGGCTGATGAGTAAATGCTTATCATCTTGAAGTGAAGGAGGAGGAGGAGGAGGAGGAG 475
QY 493 CTCTGTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 552
DB 476 CTCTGTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 535
QY 553 TAAAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 612
DB 536 TAAAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 595
QY 613 TGGGACCCGAGTACGCTAGCTAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 672
DB 596 CTGATTTAAAGCTGACAGCTAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 655
QY 673 GTGAAATGCTAGATATAGAGAGAGATCAGTGGCGAGGAGGAGGAGGAGGAGGAGGAGG 732
DB 656 GTGAAATGCTAGATATAGAGAGAGATCAGTGGCGAGGAGGAGGAGGAGGAGGAGGAGG 715
QY 733 TGACACTGAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 792
DB 716 TGACACTGAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 775
QY 733 CGTAAACGATGCTACTAGCGCTGG--GTGTATATAGTATGAGGAGGAGGAGGAGGAGG 850
DB 776 CGTAAACGATGCTACTAGCGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 835
QY 851 TGAATTC-AGCGCGGAGCGGCTGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 910

DB 836 TAAGTGAACGCGCTGGGAGGAGTACGCGCCAGAGGTTAAACCTCAATGATTAAGGAGGCGC 895
QY 911 CCGCACAACCGGTGAGGAGCTGTGCTTAAATGGAAGCAACCGGAGAACTTACTACTC 970
DB 896 CCGCACAACCGGTGAGGAGCTGTGCTTAAATGGAAGCAACCGGAGAACTTACTACTC 955
QY 971 TTGACATCCAGAAACATTTGAGAGATGAGATGAGTGGCTTGGGAGGAGTGGAGGAGGAG 1030
DB 956 TTGACATCCAGAACTTCCAGAGATGAGATGAGTGGCTTGGGAGGAGTGGAGGAGGAG 1015
QY 1031 CTGATGCTGTGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1090
DB 1016 CTGATGCTGTGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1075
QY 1091 ACCCTGTCTTATTTGCGAGAGCGTAAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1150
DB 1076 ACCCTGTCTTATTTGCGAGAGCGTAAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1135
QY 1151 AACCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1210
DB 1136 AACCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1195
QY 1211 CGCTCTCAATGCGCTTACAGAGGCTGCAAGCTAGGAGGAGGAGGAGGAGGAGGAGGAGG 1270
DB 1196 CGCTCTCAATGCGCTTACAGAGGCTGCAAGCTAGGAGGAGGAGGAGGAGGAGGAGGAGG 1255
QY 1271 GTAGCTGATGCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1330
DB 1256 ACCGATGATGATGCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1315
QY 1331 ATGCTGAATCAGATGCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1390
DB 1316 ATGCTGAATCAGATGCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1375
QY 1391 ACCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1450
DB 1376 ACCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1433
QY 1451 ACCGAGTGTCAATGAGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1483
DB 1434 ACCGAGTGTCAATGAGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1466

RESULT 9
US-09-791-610-1
Sequence 1, Application US/09791610
Publication No. US20030100084A1
GENERAL INFORMATION:
APPLICANT: Canon Inc.
TITLE OF INVENTION: Polyhydroxyalkanoate containing 3-hydroxybenzoylalkanoic acid
FILE REFERENCE: 4396021
CURRENT APPLICATION NUMBER: US/09/791,610
CURRENT FILING DATE: 2002-09-30
NUMBER OF SEQ ID NOS: 1
SEQ ID NO: 1
LENGTH: 1501
TYPE: DNA
ORGANISM: Pseudomonas jessenii 161 strain.
US-09-791-610-1

Query Match 76.1%; Score 1131; DB 11; Length 1501;
Best Local Similarity 88.2%; Pred. No. 1e-298;
Matches 1299; Conservative 0; Mismatches 165; Indels 9; Gaps 6;

QY 13 TGAACGCTGGCGGAGGCTTAAACACATGCAAGTCAAGCGGTAAACAGGGGAGCTTCTCC 72
DB 1 TGAACGCTGGCGGAGGCTTAAACACATGCAAGTCAAGCGGTAAACAGGGGAGCTTCTCC 58
QY 73 TGCTGACGAGCGGCGGAGCGGTGAGTAAACGCTAGAGATCTGCTAGTAGAGGGGAGCA 132
DB 59 TGAATTC-AGCGCGGAGCGGCTGAGTATGCTAGATCTGCTAGTAGAGGGGAGCA 117

QY 133 CATGTGAAAACGATGCTAATATCCGCATACGCCCTGAGGGGAAAAGGAGGGAGACTTTG 192
 Db 118 CCGTCGAAAAGGAGGAGCTAATACCGCAATCGCTCAGGAGAAAAGCAGGGGA--CCTTC 175
 QY 193 GAGCCTTCGGCTAATTAGATAGAGCTGCGTGAATTAAGTAAGTTAGTGGTAAAGGCTTA 252
 Db 176 GGGCCTTCGGCTAATGATGAGCCTAGGCTGGAATTAAGTAAGTTAGTGGTAAAGGCTTA 235
 QY 253 CCAAGGCGACGATCTCTAAGTGTGAGAGGATGAGCAGTCACTGGGAGCTGAGAGAC 312
 Db 236 CCAAGGCGACGATCTCTAAGTGTGAGAGGATGAGCAGTCACTGGGAGCTGAGAGAC 295
 QY 313 GGCACGACTCCTACGAGGAGGAGCAGTGGGAAATATTGACAAATGGGCGCAAGCCTGAT 372
 Db 296 GGTCCAGACTCTCTACGAGGAGGAGCAGTGGGAAATATTGACAAATGGGCGCAAGCCTGAT 355
 QY 373 CCAAGCATCCCGGCTGTGTGAAAGAGGCTTAAGGTTGTAAAGCACTTTCAGGGGTAGG 432
 Db 356 CCAAGCATCCCGGCTGTGTGAAAGAGGCTTTCGATTTGTAAAGCACTTTCAGGGGTAGG 415
 QY 433 AAGGCTATAGGTTAATAGTTATCATCTTGTAGCTTGTAGCCCGAGAAAGCAACCGGCTAA 492
 Db 416 AAGGCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 475
 QY 493 CTCTGTGCGAGAGCGCGGCTTAATACAGAGGCTGCAAGCTTAATTCGAAATTAATTCG 552
 Db 476 CTCTGTGCGAGAGCGCGGCTTAATACAGAGGCTGCAAGCTTAATTCGAAATTAATTCG 535
 QY 553 TAAAGGCGCGGCTAAGT 612
 Db 536 TAAAGGCGCGGCTAAGT 595
 QY 613 TGGCACCCTGATCTGCTAGTAGATGTGTAGAGGGGTGTGTGTGTGTGTGTGTGTGTGT 672
 Db 596 CTGCATTTCAAACTGACAAAGTATAGTATGTGTAGAGGCTGTGTGTGTGTGTGTGTGT 655
 QY 673 GTGAATTCGT 732
 Db 656 GTGAATTCGT 715
 QY 733 TGACACTGAGTGTGCGAAAGCGTGGGAGCAAAACAGATTAATATCCCTGTGTGTGTGT 792
 Db 716 TGACACTGAGTGTGCGAAAGCGTGGGAGCAAAACAGATTAATATCCCTGTGTGTGTGT 775
 QY 793 CGTAAACGATGTCTACTAGCCGTTGG--GTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 850
 Db 776 CGTAAACGATGTCTACTAGCCGTTGGAGCCCTGTGTGTGTGTGTGTGTGTGTGTGTGT 835
 QY 851 TAAGTAGACCGGCTGGGAGGTAGCGGCCGCAAGGTTAAACTCAATGATTAAGAGGGGAG 910
 Db 836 TAAGTAGACCGGCTGGGAGGTAGCGGCCGCAAGGTTAAACTCAATGATTAAGAGGGGAG 895
 QY 911 CCGCAGACGCGGTGAGCATGTGTGTATTGGAAGCAACGCAAGAACTTACTCTACTC 970
 Db 896 CCGCAGACGCGGTGAGCATGTGTGTATTGGAAGCAACGCAAGAACTTACTCAAGGCC 955
 QY 971 TTACATTCACAGAACTTTGAGAGATGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1030
 Db 956 TTACATTCACAGAACTTTGAGAGATGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1015
 QY 1031 CTGCATGCTGT 1090
 Db 1016 CTGCATGCTGT 1075
 QY 1091 ACCCTGTCTTATTGTGCGAGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1150
 Db 1076 ACCCTGTCTTATTGTGCGAGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1135
 QY 1151 AACCGAGAGAGGTGGGAGCAGAGTCAATGTATCTATGAGCCCTTACGAGTAAAGGCTTAC 1210
 Db 1136 AACCGAGAGAGGTGGGAGTGAAGTCAATGTATCTATGAGCCCTTACGAGTAAAGGCTTAC 1195

QY 1211 CGTGCTACATATGCGGTATATAGAGGGCTGCAAGCTAGCATAGTGTAGCGAATCCACAAA 1270
 Db 1196 CGTGCTACATATGCGGTATATAGAGGGCTGCAAGCTAGCATAGTGTAGCGAATCCACAAA 1255
 QY 1271 GTAGCTGTATGCGGATTTGAGTCTGCACTGATCTCCATGAAATGTGGAAATGCTAGTA 1330
 Db 1256 ACCGATGCTATGCGGATTCGAGCTGCAACTGATGCTGTGAATGTGGATGTAGTA 1315
 QY 1331 ATCGTAATCAGATATGACAGGTAATACCTTCCGGGCTTGTACACACCGCCGTCAC 1390
 Db 1316 ATCGTAATCAGATATGCGGATTCGAGCTGCAACTGATGCTGTGAATGTGGATGTAGTA 1375
 QY 1391 ACCATGAGGTTGATGTGCTCAGAAATGACTAGCTTAACCTTCCGGGATGGCGTTACC 1450
 Db 1376 ACCATGAGGTTGATGTGCTCAGAAATGACTAGCTTAACCTTCCGGGATGGCGTTACC 1433
 QY 1451 ACGGAGTGTCAATGACTGGGCTTGAAGTGTAC 1483
 Db 1434 ACGGAGTGTCAATGACTGGGCTTGAAGTGTAC 1466

RESULT 10
 US-10-242-696-1
 ; Sequence 1, Application US/10242696
 ; Publication No. US20030180899A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Honma, Tsutomu
 ; APPLICANT: Kobayashi, Toyoko
 ; APPLICANT: Yano, Tetsuya
 ; APPLICANT: Kobayashi, Shin
 ; APPLICANT: Imamura, Takeshi
 ; APPLICANT: Suda, Sakae
 ; APPLICANT: Kemoku, Takeshi
 ; TITLE OF INVENTION: Process for producing polyhydroxyalkanoate by utilizing microo
 ; FILE REFERENCE: 03500, 015010.1
 ; CURRENT APPLICATION NUMBER: US/10/242,696
 ; CURRENT FILING DATE: 2002-09-13
 ; PRIOR APPLICATION NUMBER: JP 11-371864
 ; PRIOR FILING DATE: 12-27-1999
 ; PRIOR APPLICATION NUMBER: JP 11-371867
 ; PRIOR FILING DATE: 12-27-1999
 ; PRIOR APPLICATION NUMBER: JP 11-371868
 ; PRIOR FILING DATE: 12-27-1999
 ; PRIOR APPLICATION NUMBER: JP 11-371869
 ; PRIOR FILING DATE: 12-27-1999
 ; PRIOR APPLICATION NUMBER: JP 2000-023024
 ; PRIOR FILING DATE: 01-31-2000
 ; PRIOR APPLICATION NUMBER: JP 2000-023025
 ; PRIOR FILING DATE: 01-31-2000
 ; PRIOR APPLICATION NUMBER: JP 2000-361323
 ; PRIOR FILING DATE: 11-28-2000
 ; NUMBER OF SEQ ID NOS: 1
 ; SOFTWARE: Microsoft Word
 ; SEQ ID NO 1
 ; LENGTH: 1501
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas jessenii P.161 ; FERM P-17445
 US-10-242-696-1

Query Match 76.1%; Score 1131; DB 13; Length 1501;
 Best Local Similarity 88.2%; Pred. No. 1e-298;
 Matches 1999; Conservative 0; Mismatches 165; Indels 9; Gaps 6;
 QY 13 TGAACGCTGGGCGGAGGCTTAAACATGCAAGTGCAGCGGTAAACAGGGAGCTTGCTCC 72
 Db 1 TGAACGCTGGGCGGAGGCTTAAACATGCAAGTGCAGCGGTAAACAGGGAGCTTGCTCC 58
 QY 73 TGTCTAGAGGCGGCGGAGGCTTAAACATGCAAGTGCAGCGGTAAACAGGGAGCTTGCTCC 132
 Db 59 TGAATTC-AGCGGGCGGAGGCTTAAACATGCAAGTGCAGCGGTAAACAGGGAGCTTGCTCC 117
 QY 133 CATGTGAAAACGATGCTAATATCCGCATACGCCCTGAGGGGAAAAGGAGGAGCTTTG 192

Db 118 GGTCTGCAAGGAGGACGCTAATACCGCATACGTCTTACGAGGAGAAAGACGGGGA--CCCTTC 175
Qy 193 GAGCCTTCGCTTATAGATGAGCTCCGCTGAGATTAAGTATGGTAGGGTAAGGCTTA 252
Db 176 GGGCCTTGCGCTATCAGATGAGCTTACGATTAAGCTTGGTAGGGTAAGGCTCA 235
Qy 253 CCAAGGCGAGATCTCTAACTGGTCTGAGAGATGACAGTCACTGGGACTGAGACAC 312
Db 236 CCAAGGCGAGATCTCTAACTGGTCTGAGAGATGATCAGTCACTGGGACTGAGACAC 295
Qy 313 GGGCCAGACTCTTACGAGGAGGACGAGTGGGAAATTGGACAAATGGCGAAAGGCTGAT 372
Db 296 GGTCCAGACTCTTACGAGGAGGACGAGTGGGAAATTGGACAAATGGCGAAAGGCTGAT 355
Qy 373 CCAAGCCTGCGCGGTGTGTAAGAGAGGCTTAAAGGCTTAAAGCACTTCAAGGAGT 432
Db 356 CCAAGCCTGCGCGGTGTGTAAGAGAGGCTTAAAGGCTTAAAGCACTTAAAGTGGAG 415
Qy 433 AAGGCTGATAGTTAATACGTTATCATTGACGTTAGCCCGAAGAAAGCAACGGCTTA 492
Db 416 AAGGCTGATAGTTAATACGTTATGAGTTAGGTTAGCCGACAGAAATAGCACCGGCTTA 475
Qy 493 CTCTGTGCGCAGACCGCGGCTTATACAGAGGCTGACAGGCTTAACTCGAACTTACTGG 552
Db 476 CTCTGTGCGCAGACCGCGGCTTATACAGAGGCTGACAGGCTTAACTCGAACTTACTGG 535
Qy 553 TAAAGCGCGGATGATGTTTGTAAAGTGGATGTAATCCAGAGGCTCAACTTGGAA 612
Db 536 TAAAGCGCGGATGATGTTTGTAAAGTGGATGTAATCCAGAGGCTCAACTTGGAA 595
Qy 613 TGGGACCCGATCTGGTACGTAAGTATGTAAGAGGCTGTAATTTCTGTGTACG 672
Db 596 CTGCTATCAAACTGAAAGCTGAGATGTAAGAGGCTGTAATTTCTGTGTACG 655
Qy 673 GTGAAATGCGTATATAGGAAAGAAATCAGTGGGAGGACGACACCTGAGCTAATAC 732
Db 656 GTGAAATGCGTATATAGGAAAGAAATCAGTGGGAGGACGACACCTGAGCTAATAC 715
Qy 733 TGACACTGAGGTGCGAAAGGCTGGGAGGACAAAGATTAATCCTGTGTACGCGC 792
Db 716 TGACACTGAGGTGCGAAAGGCTGGGAGGACAAAGATTAATCCTGTGTACGCGC 775
Qy 793 CGTAAAGATGCTACTAGCCGTTGG--GTGTAAATGACTGTGGCGAGCTAAGCGAA 850
Db 776 CGTAAAGATGCTACTAGCCGTTGG--GTGTAAATGACTGTGGCGAGCTAAGCGAA 835
Qy 851 TAAAGTACCGCTGGGAGGTAGCGCCGCAAGGTTAAATCTCAATGAATTGACGCGG 910
Db 836 TAAAGTACCGCTGGGAGGTAGCGCCGCAAGGTTAAATCTCAATGAATTGACGCGG 895
Qy 911 CCGCAAGCGGTGAGACATGTGTTTAAATTCAGAACAGCGGAACCTTAATCTACTC 970
Db 896 CCGCAAGCGGTGAGACATGTGTTTAAATTCAGAACAGCGGAACCTTAATCTACTC 955
Qy 971 TTGACATCCAGAAACATTTGAGAGATCAGATGTTGCTTCGGAATCTGTGAGAGGTG 1030
Db 956 TTGACATCCAGAAACATTTGAGAGATGAGATGTTGCTTCGGAATCTGTGAGAGGTG 1015
Qy 1031 CTGATGCTGTCTGCTGAGCTGTGTGTAATGTTGGTTAAATGCTCCGTTAAGAGCGCA 1090
Db 1016 CTGATGCTGTCTGCTGAGCTGTGTGTAATGTTGGTTAAATGCTCCGTTAAGAGCGCA 1075
Qy 1091 ACCCTGTCTTATTTGGCAGCAGTAAATGTTGGGAACTTAAAGGAGCTGCGCGGAGCA 1150
Db 1076 ACCCTGTCTTATTTGGCAGCAGTAAATGTTGGGAACTTAAAGGAGCTGCGCGGAGCA 1135
Qy 1151 AACCGAGAGAGTGGGAGCAGCGTCAAGTATCATGAGCCCTTACAGATGAGGCTTACACA 1210
Db 1136 AACCGAGAGAGTGGGAGTACGTCATGATCATGAGCCCTTACAGGCTGAGCTTACACA 1195
Qy 1211 CGTGTATCAATGGGCTATACAGAGGCTGAGAGCTTACAGTATGAGCGGAATCCACAA 1270
Db 1196 CGTGTATCAATGGGCTATACAGAGGCTTACAGAGCTTACAGTATGAGCTTACACA 1255

Qy 1271 GTACGCTGATGCGCGATTTGAGTCTGCACTGCACTCAATGAAGTGGATCGTATGA 1330
Db 1256 ACCGATCGTATGCGCGATTCGAGTCTGCACTGCGGATGAGTGGATCGTATGA 1315
Qy 1331 ATCGTGAATCAGATGTCACGCTGTAATCGTTCCCGGCGCTTGTATCACACCGCGCTCAC 1390
Db 1316 ATCGGGAATCAGAAATGTCGCGTGAATACGTTCCCGGCGCTTGTATCACACCGCGCTCAC 1375
Qy 1391 ACCATGGAGTGAATGCTCCAGAAATGATGCTTAACCTTCGGGAGATGCGGCTTACC 1450
Db 1376 ACCATGGAGTGAATGCTCCAGAAATGATGCTTAACCTTCGGGAGATGCGGCTTACC 1433
Qy 1451 ACGGATGCTCAATGATGCGGCTTGAAGCTTAC 1483
Db 1434 ACGGATGCTCAATGATGCGGCTTGAAGCTTAC 1466

RESULT 11
US-10-411-319-1
; Sequence 1, Application US/10411319
; Publication No. US20030208029A1
; GENERAL INFORMATION:
; APPLICANT: Canon Inc.
; TITLE OF INVENTION: Polyhydroxamate, Method For Production Thereof And Microorganism
; FILE REFERENCE: 03500.015001.1
; CURRENT APPLICATION NUMBER: US/10/411.319
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US 09/748,205
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii 161 strain
US-10-411-319-1

Query Match 76.1%; Score 1131; DB 13; Length 1501;
Best Local Similarity 88.2%; Pred. No. 1e-298;
Matches 1299; Conservative 0; Mismatches 165; Indels 9; Gaps 6;

Qy 13 TGAAGCGTGGCGGACGCTTAAACATAGCAAGTGCAGCGGTTAACAGGGGAGCTTGCTCC 72
Db 1 TGAAGCGTGGCGGACGCTTAAACATAGCAAGTGCAGCGGTTAACAGGGGAGCTTGCTCC 58
Qy 73 TGCTGACAGCGCGCGAGCGGTGAGTAAACGCTGAGAAATCTGCTTATGAGGGGACAA 132
Db 59 TGAATTC-AGCGGCGGACGGGTGAGTAAATGCTTGAAGATCTGCTGTATGTTGGGAGCAA 117
Qy 133 CATGTGAAACGATGCTAATACCGCATACCGCTGAGAGGAGAAAGAGGGGAGACTTCTCG 192
Db 118 GGTCTGAAAGGAGCGCTAATACCGCATACCGCTGAGAGGAGAAAGAGGGGAGACTTCTCG 175
Qy 193 GAGCCTTCGCTTATGATGAGCTGCTGATTAATGATTAATGTTGGTTAAAGGCTTA 252
Db 176 GGGCCTTGCGCTATCAGATGAGCTTACGATTAATGATTAATGTTGGTTAAAGGCTTA 235
Qy 253 CCAAGGCGAGATCTTAACTGGTCTGAGAGATCAACAGTACACTGGGACTGAGACAC 312
Db 236 CCAAGGCGAGATCTTAACTGGTCTGAGAGATCAACAGTACACTGGGACTGAGACAC 295
Qy 313 GGGCCAGACTCTTACGAGGAGGACAGTGGGAAATTGGACAAATGGCGAAAGGCTGAT 372
Db 296 GGTCCAGACTCTTACGAGGAGGACAGTGGGAAATTGGACAAATGGCGAAAGGCTGAT 355
Qy 373 CCAAGCCTGCGCGGTGTGTAAGAGGCTTAAAGGCTTAAAGCACTTCAAGGAGT 432
Db 356 CCAAGCCTGCGCGGTGTGTAAGAGGCTTAAAGGCTTAAAGCACTTAAAGTGGAGG 415
Qy 433 AAGGCTGATAGTTAATACGTTATCATTGACGTTAGCCCGAAGAAAGCAACGGCTTA 492

416 AAGGCATTAACTAATAGTGTAGTGTGACGTACCGACAGAAATTAAGCAGCGCTAA 475
 493 CTCTGTCCAGCAGCCCGGGTAAATACAGAGGGTCCAGCGTTAATCGGAATTCCTGGGG 552
 476 CTCTGTCCAGCAGCCCGGGTAAATACAGAGGGTCCAGCGTTAATCGGAATTCCTGGGG 535
 553 TAAAGCGCGGTAGGTGTGTTTAAAGTCGAGTGTGAATCCAGGGCTCAACCTTGGAA 612
 536 TAAAGCGCGGTAGGTGTGTTTAAAGTCGAGTGTGAATCCAGGGCTCAACCTTGGAA 595
 613 TGGCACCAGATCTGGCTAGCTAGATGTGTAGAGGGGTGTGAATTTCTGTGTAGCG 672
 536 CTGCATTCAAACTACACAGCTAGAGTGTGTAGAGGGGTGTGAATTTCTGTGTAGCG 655
 673 GTGAATGCGTATATATATAGAGAAATCATAGTGGCGAAGCGCACCTGTAGTATATAC 732
 656 GTGAATGCGTATATATAGAGAAATCATAGTGGCGAAGCGCACCTGTAGTATATAC 715
 733 TGACACTGAGGTGCGAAAGCGTGGGAGCAAAACAGATTAGATCCCTGTAGTCCAGCG 792
 716 TGACACTGAGGTGCGAAAGCGTGGGAGCAAAACAGATTAGATCCCTGTAGTCCAGCG 775
 793 CGTAACGATGTCTACTGACCGCTGG--GTGTATATGACTTATAGTGGCGAGCTTAAGCGAA 850
 776 CGTAACGATGTCTACTGACCGCTGGAGCCTTATAGTGTGGCGAGCTTAAGCGAA 835
 851 TAAGTAGACCGCGCTGGAGTACGCGCCAGAGTTAAACTCAATATGATGAAGGGGG 910
 836 TAAGTAGACCGCGCTGGAGTACGCGCCAGAGTTAAACTCAATATGATGAAGGGGG 895
 911 CCGCAACAGCGGTGAGATGTGTTTAAATTCGAAGCAACCGAAAGAACTTACCTACTC 970
 896 CCGCAACAGCGGTGAGATGTGTTTAAATTCGAAGCAACCGAAAGAACTTACCGAGCC 955
 971 TTGACATCCAGCAATTTGAGAGATCAGATGGGCTTGGGAGCTGTGAGACAGGTG 1030
 956 TTGACATCCAGCAATTTGAGAGATCAGATGGGCTTGGGAGCTGTGAGACAGGTG 1015
 1031 CTGCAATGCTGTGTCACTGTGTGTGAAATGTTGGGTTAAGTCCCGTAACGAGCGCA 1090
 1016 CTGCAATGCTGTGTCACTGTGTGTGAAATGTTGGGTTAAGTCCCGTAACGAGCGCA 1075
 1091 ACCCTTGTCTTATTTGGCAGACGATATGTTGGGAACTTAAAGAGACTGGCGGTAGCA 1150
 1076 ACCCTTGTCTTATTTGGCAGACGATATGTTGGGAACTTAAAGAGACTGGCGGTAGCA 1135
 1151 AACCGAGAGAGGTGGGAGCAAGCTCAAGTATCATGAGCCCTTACGAGTGGGTACACA 1210
 1136 AACCGAGAGAGGTGGGAGTACAGTCAAGTATCATGAGCCCTTACGAGTGGGTACACA 1195
 1211 CGTGTACATAGGCGTATACAGAGGGCTGCAAGCTAGAGTATGAGCGGAATCCCAAAA 1270
 1196 CGTGTACATAGGCGTATACAGAGGGTTCAGAGCCGAGGTGAGTATCCCAAAA 1255
 1271 GTACGTCTAGTCCGAGTTGAGGTCTGCAACTGCACTCAGTGAAGTGGAACTGCTAGTA 1330
 1256 ACCGATCTAGTCCGAGTTCGAGTCTGCAACTGCACTCAGTGAAGTGGAACTGCTAGTA 1315
 1331 ATCTGTAATCAGAAATGTCAAGGTGAATACTTCCGGGCTTGTACACACCGCCGTAC 1390
 1316 ATCTGTAATCAGAAATGTCAAGGTGAATACTTCCGGGCTTGTACACACCGCCGTAC 1375
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 1376 ACCATGGAGTGTGATTTGCTCCAGAGTGTAGTACTTAACTTGGGGATGGGGGTATAC 1433
 1451 ACGGAGTGTGATGATGCTGGGGTGAAGTCTAC 1483
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RESULT 12
 US-10-218-519-5

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; Sequence 5, Application US/10218519
; Publication No. US2003049806A1
; GENERAL INFORMATION:
; APPLICANT: Yano, Tetsuya
; APPLICANT: Imamura, Takeshi
; APPLICANT: Suda, Sakae
; APPLICANT: Homma, Tsutomu
; TITLE OF INVENTION: Polyhydroxyalkanoate Synthase and Gene Encoding the Same Enzyme
; FILE REFERENCE: 03500.015225.1
; CURRENT APPLICATION NUMBER: US/10/218,519
; CURRENT FILING DATE: 2001-03-30
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Microsoft Word
; SEQ ID NO 5
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii Pl61 ; BP-7376
; FEATURE:
; FEATURE: cDNA to 16S rRNA
US-10-218-519-5

Query Match      76.1%; Score 1131; DB 15; Length 1501;
Beet Local Similarity 88.2%; Pred. No. 1e-298;
Matches 1299; Conservative 0; Mismatches 165; Indels 9; Gaps 6;

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373 CCAAGCGAGAGATCTTAATCTGCTGAGAGATGACCACTGCACTGGGACTGAGACAC 432
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 Db 776 GGTAAACGATGTCTACGACCGCTTGAGACCTTGTAGTGGCCAGCTAACGAT 835
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 Db 836 TAAATGACCGCTGGGGAGTAGCGCCGCAAGTTAACTCAATTGATGACGGGGC 895
 Qy 911 CCGACAGCGGTGGAGCATGTGTGTTAATTGAAAGCAACGGAGAACCTTACCTACTC 970
 Db 896 CCGACAGCGGTGGAGCATGTGTGTTAATTGAAAGCAACGGAGAACCTTACCGAGCC 955
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 Db 1434 ACCGAGTGTCAATGACTGGGGTTGAAGTCTAC 1466

RESULT 13
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 ; Sequence 5, Application US/10266787
 ; Publication No. US20030082777A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yano, Tetsuya
 ; APPLICANT: Imamura, Takeshi
 ; APPLICANT: Suda, Sakae
 ; APPLICANT: Horima, Tsutomu
 ; TITLE OF INVENTION: Polyhydroxyalcanate Synthase and Gene Encoding the Same Enzyme
 ; FILE REFERENCE: 03500.015225.3
 ; CURRENT APPLICATION NUMBER: US/10/266.787
 ; CURRENT FILING DATE: 2002-10-09
 ; PRIOR APPLICATION NUMBER: JP 2000-095004
 ; PRIOR FILING DATE: 2000-03-30
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: Microsoft Word
 ; SEQ ID NO 5

; LENGTH: 1501
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas jessenii P161 ; BP-7376
 ; FEATURE:
 ; FEATURE: cDNA to 16S rRNA
 ; US-10-266-787-5
 Query Match 76.1%; Score 1131; DB 15; Length 1501;
 Best Local Similarity 89.2%; Pred. No. 1e-298;
 Matches 1299; Conservative 0; Mismatches 165; Indels 9; Gaps 6;
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 Db 118 CGTCTGAAAGGAGCGCTAATATACCGCATACCGCTCTACGGGAAAGAGGAGGGA--CCTTC 175
 Qy 193 GAGCCTTCGCTATTAGATGAGCTGCTGCTGAGATTACCTGTTGGTGAAGGCTTA 252
 Db 176 GGGCCTTGGGCTATGAGATGAGCTGAGTCCGATTACCTGTTGGTGAAGGCTTA 235
 Qy 253 CCAAGGCGAGATCTCTAATGCTCTGAGAGATGACCACTGACCTGAGACTGAGACAC 312
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 Qy 313 GGCCGAGACTCTTACGAGAGGAGCAGAGTGGGGAATTTGGCAATGGGCCAGCTGAT 372
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 Qy 433 AAGGCTGATAGGTAAATCGTTATCTTACGCTTGAAGCCCGAGAGAGCAGCCGCTAA 492
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 Qy 613 TGGCACCGCATCTGGCTAGCTAGATGTGTAAAGGGGTGTGAATTTCTGTGTAGCG 672
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 Qy 673 GTGAATGCGTAGATATAGAAAGCACTACGTGCGAGGCGACACCTTGAATTAATAC 732
 Db 656 GTGAATGCGTAGATATAGAAAGCACTACGTGCGAGGCGACACCTTGAATTAATAC 715
 Qy 733 TGAACCTGAGGTGCGAAGCGTGGGAGCAAAACAGATTAGATACCTGGTAGTCACGC 792
 Db 716 TGAACCTGAGGTGCGAAGCGTGGGAGCAAAACAGATTAGATACCTGGTAGTCACGC 775
 Qy 793 CGTAAACGATGTCTACGACCGCTTG--GTTGTAATGACTTGTGGCGAGCTAACGCA 850
 Db 776 CGTAAACGATGTCTACGACCGCTTGGAGCCTTGAAGCTTGAAGGCGAGCTAACGAT 835
 Qy 851 TAAATGACCGCTGGGAGTAGCGCCGCAAGTTAACTCAATTGATGACGGGGC 910
 Db 836 TAAATGACCGCTGGGAGTAGCGCCGCAAGTTAACTCAATTGATGACGGGGC 895
 Qy 911 CCGACAGCGGTGAGAGATGTGTTAATGGAAGCAACGGAAGACCTTACCTACTC 970

Db 1434 ACGGTGATTCATGACTGGGTCGAAGTCGTAC 1466

Search completed: January 31, 2004, 00:02:23
Job time : 570.517 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 30, 2004, 14:49:24 ; Search time 4084.5 Seconds

(without alignments)
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Scoring table: IDENTITY NUC

Gapop 10-0, Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

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and is derived by analysis of the total score distribution.

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6	1057.6	98.8	1452	1	AY014828 Pseudomon
7	1057.2	98.8	1461	1	AF388208 Pseudomon
8	1057.2	98.8	1451	1	AY014824 Pseudomon
9	1056.6	98.7	1355	1	AF094729 Pseudomon
10	1056.4	98.7	1140	6	AX175617 Sequence
11	1056.4	98.7	1500	1	AF267911 Pseudomon
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34	1038.4	97.0	1477	1	AF094738 Pseudomon
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36	1037.2	96.9	1449	1	AY014814 Pseudomon
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ALIGNMENTS

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LOCUS AX175614 1070 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 2 from Patent WO0144275.
ACCESSION AX175614
VERSION AX175614.1 GI:14598934
KEYWORDS
SOURCE Pseudomonas sp.
ORGANISM Pseudomonas sp.
REFERENCE 1
AUTHORS Berry,M.J., Griffiths,A.U., Hill,P.J., Laybourne-Parry,J. and
TITLE Processes and organisms for the production of anti-freeze proteins
JOURNAL Patent: WO 0144275-A 2 21-JUN-2001;

QY 363 GCCTGATCCAGCCATGCGCGTGTGTAAGAAGTCTTGAGATTGTAAGCACTTAAAGT 422
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 ACCESSION AY014815
 VERSION AY014815.1 GI:17220733
 KEYWORDS
 SOURCE Pseudomonas sp. NZ065
 ORGANISM Pseudomonas sp. NZ065
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 Pseudomonadaceae; Pseudomonas.
 REFERENCE 1 (bases 1 to 1458)
 AUTHORS Godfrey,S.A.C., Harrow,S.A., Marshall,J.W. and Klena,J.D.
 TITLE Characterization of Pseudomonas species (sensu stricto) causing
 'ginger biotch' disease of cultivated Agave species using 16S
 rRNA gene typing
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1458)
 AUTHORS Godfrey,S.A.C., Harrow,S.A., Marshall,J.W. and Klena,J.D.
 TITLE Direct Submission
 JOURNAL Submitted (28-NOV-2000) Integrated Crop Protection, Crop & Food
 Research Ltd., Private Bag 4704, Christchurch 8152, New Zealand
 FEATURES Location/Qualifiers

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 /db_xref="taxon:148756"
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 BASE COUNT 373 a 323 c 451 g 311 t
 ORIGIN
 Query Match 98.9%; Score 1058; DB 1; Length 1458;
 Best Local Similarity 99.5%; Pred. No. 0;
 Matches 1061; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 rRNA
 QY 3 CCTTGCTCAGATTGAACGCTGCGAGCGCTTAACATGCAATGCAAGTCGAGCGGTAGAGAGA 62
 Db 11 CTTGGCTCAGATTGAACGCTGCGAGCGCTTAACATGCAATGCAAGTCGAGCGGTAGAGAGA 70
 QY 63 AGCTTGCTTCTCTTGAGAGCGCGGAGCGGTGAGTAAATGCTTAGAATCTGCTGTAGT 122
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 QY 123 GGGGAAATAAGTTCGGAACGAGCGCTAATACCGATAGTCTACGGGAAAGCAGG 182
 Db 131 GGGGAAATAAGTTCGGAACGAGCGCTAATACCGATAGTCTACGGGAAAGCAGG 190
 QY 183 GACCTTGCGGCTTTCGCTATGATGAGCTAGTGGTGAATTAAGCTTGTGAGTTAA 242
 Db 191 GACCTTGCGGCTTTCGCTATGATGAGCTAGTGGTGAATTAAGCTTGTGAGTTAA 250
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 Db 491 CGGCTAACTGTGTCCAGACGCGCGTATATACAGAGGGTGAAGGGTAAATCGAATTA 550
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QY 903 CGGGGGCCCCGACAGCGGTGGAGCATGTGTTTAATTCAGAACACGCGAAGACCTTA 962
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RESULT 4
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 DEFINITION AY014823
 ACCESSION AY014823
 VERSION AY014823.1 GI:17220741
 KEYWORDS
 SOURCE Pseudomonas sp. NZ106
 ORGANISM Pseudomonas sp. NZ106
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 Pseudomonadaceae; Pseudomonas.
 REFERENCE 1 (bases 1 to 1467)
 Godfrey, S.A.C., Harrow, S.A., Marshall, J.W. and Klena, J.D.
 Characterization of Pseudomonas species (sensu stricto) causing
 'finger blotch' disease of cultivated Agaricus bisporus using 16S
 rRNA gene typing
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1467)
 Godfrey, S.A.C., Harrow, S.A., Marshall, J.W. and Klena, J.D.
 Direct Submission
 TITLE Submitted (28-NOV-2000) Integrated Crop Protection, Crop & Food
 JOURNAL Research Ltd., Private Bag 4704, Christchurch 8152, New Zealand
 FEATURES
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 BASE COUNT 373 a 323 c 455 g 316 t
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Query Match 98.9%; Score 1058; DB 1; Length 1467;
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 QY 123 GGGGGAATAAGTTCGGAACGAGCCTAATACCGCATACGCTCTACCGGAGAAAGCAGG 182
 Db 131 GGGGGAATAAGTTCGGAACGAGCCTAATACCGCATACGCTCTACCGGAGAAAGCAGG 190
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 Db 191 GACCTTGGGCTTGGCTGATAGATGAGCTTAGGCTGATTAATGCTGTGAGGTAA 250
 QY 243 TGGCTCACCAAGACGATCGCTAGCTGCTGAGAGATGATCACTGCACTGGAAGT 302
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Db 311 GAGACAGGCTCCAGACTCTTACGAGAGGAGCAGAGATGTGGGAATATTGACAAATGGCGAAA 370
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 Db 371 GCTGATCCAGCCATGCGCGGTGTGTGAAGAGGCTTGTGATTTGTAAGCCTTAAGT 430
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RESULT 5
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 LOCUS Pseudomonas sp. NZ066 16S ribosomal RNA gene, partial sequence.
 DEFINITION AF388209
 ACCESSION AF388209
 VERSION AF388209.1 GI:18150371
 KEYWORDS
 ORGANISM Pseudomonas sp. NZ066
 SOURCE Pseudomonas sp. NZ066
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 Pseudomonadaceae; Pseudomonas.
 REFERENCE 1 (bases 1 to 1452)
 Godfrey, S.A., Harrow, S.A., Marshall, J.W. and Klena, J.D.
 Characterization by 16S rRNA sequence analysis of pseudomonads
 causing blotch disease of cultivated Agaricus bisporus
 JOURNAL Appl. Environ. Microbiol. 67 (9), 4316-4323 (2001)
 MEDLINE 21417060
 PUBMED 11526038
 REFERENCE 2 (bases 1 to 1452)
 Godfrey, S.A.C., Harrow, S.A., Marshall, J.W. and Klena, J.D.
 Direct Submission
 TITLE Submitted (04-JUN-2001) Integrated Crop Protection, New Zealand
 JOURNAL

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 Db 911 CGGGGGCCCGACAGCGGTGAGACATGTGTTAATTCGAACCAACGGAAGACCTTA 970
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 Db 1031 ACAGGTGCTGATGCTGTGCTGAGCTCGTGTGTGTAATGTAG 1076

RESULT 7
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 LOCUS Pseudomonas sp. NZ064 16S ribosomal RNA gene, partial sequence.
 DEFINITION AF388208
 ACCESSION AF388208 GI:18150370
 VERSION AF388208.1
 KEYWORDS
 SOURCE Pseudomonas sp. NZ064
 ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 Pseudomonadaceae; Pseudomonas.
 REFERENCE 1 (bases 1 to 1461)
 AUTHORS Godfrey, S.A., Harrow, S.A., Marshall, J.W. and Klens, J.D.
 TITLE Characterization by 16S rRNA sequence analysis of Pseudomonas
 causing blotch disease of cultivated Agaricus bisporus
 JOURNAL Appl. Environ. Microbiol. 67 (9), 4316-4323 (2001)
 MEDLINE 21417060
 PUBMED 11526038
 REFERENCE 2 (bases 1 to 1461)

AUTHORS Godfrey, S.A.C., Harrow, S.A., Marshall, J.W. and Klens, J.D.
 TITLE Direct Submission
 JOURNAL Submitted (04-JUN-2001) Integrated Crop Protection, New Zealand
 Institute for Crop & Food Research Ltd, Private Bag 4704,
 Christchurch, New Zealand
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 Best Local Similarity 99.3%; Pred. No. 0;
 Matches 1059; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
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 QY 603 CTGGGAATGCACTTCAAACTGACTGACTAGATAGTATGATGAGGTTGTTGAATTTCTG 662
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 QY 663 TGTAGCGGTGAATGCGTATATATAGAAAGAACACCAATGGCGAAGCCACCTTGA 722
 Db 671 TGTAGCGGTGAATGCGTATATATAGAAAGAACACCAATGGCGAAGCCACCTTGA 730
 QY 723 CTAAATCTGACACTGAGGTGGGAAAGGTGGGGGCAAAACAGATTAGTACCTTGTG 782
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/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1
/ LENGTH: 1501
/ TYPE: DNA
/ ORGANISM: Pseudomonas jessenii 161 strain
US-10-411-319-1
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Query Match      92.1%; Score 985.2; DB 13; Length 1501;
Best Local Similarity 95.9%; Pred. No. 1.3e-292;
Matches 1011; Conservative 0; Mismatches 43; Indels 0; Gaps 0;
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DB 61 AATTCAAGCGCGAGCGGTAGATGCTAGAGATCTGCTGATGAGGGGATTAAGT 120
QY 135 TCGAAAACGAGCGCTTAATACCGCATACGCTTACCGGAGAAAGCAGGCGACCTTCGAGGC 194
DB 121 CTCGAAAAGGAGCGCTAATACCGCATACGCTTACCGGAGAAAGCAGGCGACCTTCGAGGC 180
QY 195 TTGCGCTATCAGATAGAGCTAGGTGAGTTAGTTAGTTGAGTGAAGTCACTCAAG 254
DB 181 TTGCGCTATCAGATAGAGCTAGGTGAGTTAGTTAGTTGAGTGAAGTCACTCAAG 240
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QY 455 TCCAGAGCAGCGCGGTAAATACAGAGGAGTGAAGGTTATGCGAATTAAGTGGCGGTAAG 554
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RESULT 14
US-10-218-519-5
/ Sequence 5, Application US/10218519
/ Publication No. US20030049806A1
/ GENERAL INFORMATION:
/ APPLICANT: Yano, Tetsuya
/ APPLICANT: Imamura, Takeshi
/ APPLICANT: Suda, Sakae
/ APPLICANT: Honma, Tsutomu
/ TITLE OF INVENTION: Polyhydroxyalkanoate Synthase and Gene Encoding the Same Enzy
/ FILE REFERENCE: 03500.015225.1
/ CURRENT FILING DATE: 2001-03-30
/ PRIOR APPLICATION NUMBER: 09/821,016
/ PRIOR FILING DATE: 2001-03-30
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: Microsoft Word
/ SEQ ID NO 5
/ LENGTH: 1501
/ TYPE: DNA
/ ORGANISM: Pseudomonas jessenii P161 ; BP-7376
/ FEATURE:
/ FEATURE: CDNA to 16S rRNA
US-10-218-519-5
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Best Local Similarity 95.9%; Pred. No. 1.3e-292;
Matches 1011; Conservative 0; Mismatches 43; Indels 0; Gaps 0;
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DB 961 ATCCAAATGAATCTTTCTAGAGATGATGTTGCTTGGGAACTTTAGAGACAGGTGCTGCA 1020
QY 1035 TGGCTGTGCTGAGCTGCTGTTGTAATGTATAG 1068
DB 1021 TGGCTGTGCTGAGCTGCTGTTGTAATGTATAG 1054

RESULT 12
US-10-242-696-1
; Sequence 1, Application US/10242696
; Publication No. US20030180899A1
; GENERAL INFORMATION:
; APPLICANT: Honma, Tsutomu
; APPLICANT: Kobayashi, Toyoko
; APPLICANT: Yano, Tetsuya
; APPLICANT: Kobayashi, Shin
; APPLICANT: Imamura, Takeshi
; APPLICANT: Suda, Sakae
; APPLICANT: Kenmoku, Takashi
; TITLE OF INVENTION: Process for producing polyhydroxyalkanoate by utilizing microorga
; FILE REFERENCE: 03500.015010.1
; CURRENT APPLICATION NUMBER: US/10/242, 696
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: JP 11-371864
; PRIOR FILING DATE: 12-27-1999
; PRIOR APPLICATION NUMBER: JP 11-371867
; PRIOR FILING DATE: 12-27-1999
; PRIOR APPLICATION NUMBER: JP 11-371868
; PRIOR FILING DATE: 12-27-1999
; PRIOR APPLICATION NUMBER: JP 11-371869
; PRIOR FILING DATE: 12-27-1999
; PRIOR APPLICATION NUMBER: JP 2000-023024
; PRIOR FILING DATE: 01-31-2000
; PRIOR APPLICATION NUMBER: JP 2000-023025
; PRIOR FILING DATE: 01-31-2000
; PRIOR APPLICATION NUMBER: JP 2000-361323
; PRIOR FILING DATE: 11-28-2000
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Microsoft Word
; SEQ ID NO 1
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii P161 ; FERM P-17445
US-10-242-696-1

Query Match 92.1%; Score 985.2; DB 13; Length 1501;
Best Local Similarity 95.9%; Pred. No. 1.3e-292;
Matches 1011; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 15 TGAACGCTGGCGGAGGCTTAACATGCAAGTCAGAGGTAGAGAGAGCTTCTC 74
DB 1 TGAACGCTGGCGGAGGCTTAACATGCAAGTCAGAGGTAGAGAGAGCTTCTC 60
QY 75 TTGAGAGCGGCGGAGGCTTAATGCTTAGAATCTGCTGTGATGGGGATAAGT 134
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DB 181 TTGCGCTATCAGATGAGCTTAGTGGATTAAGCTAAGTTGATGAGATTAATGGCTACCAAG 240
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DB 961 ATCCAAATGAATCTTTCTAGAGATGATGTTGCTTGGGAACTTTAGAGACAGGTGCTGCA 1020
QY 1035 TGGCTGTGCTGAGCTGCTGTTGTAATGTATAG 1068
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RESULT 13
US-10-411-319-1
; Sequence 1, Application US/10411319
; Publication No. US20030208029A1
; GENERAL INFORMATION:
; APPLICANT: Canon Inc.
; TITLE OF INVENTION: Polyhydroxamate, Method For Production Thereof And Microorganism
; FILE REFERENCE: 03500.015001.1
; CURRENT APPLICATION NUMBER: US/10/411, 319
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US 09/748, 205
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 1

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QY      135 TCGAAAACGGACGCTAATACCGCATACGCTTACGGGAGAAAGAGGAGACCTTCGGGCC 194
Db      121 CTCGAAAGGAGCGCTAATACCGCATACGCTTACGGGAGAAAGAGGAGACCTTCGGGCC 180
QY      195 TTGGCGCTACAGATGAGCGCTAGTGGAGTTAGCTAGTGGAGGATATGGCTTACCAAC 254
Db      181 TTGGCGCTACAGATGAGCGCTAGTGGAGTTAGCTAGTGGAGGATATGGCTTACCAAC 240
QY      255 GCGAGCATCCGTAACCTGCTGAGAGATGATCAGTCACTGAGACTGAGACAGCTCC 314
Db      241 GCGAGCATCCGTAACCTGCTGAGAGATGATCAGTCACTGAGACTGAGACAGCTCC 300
QY      315 AGACTCTACGAGGAGCGAGCTGGGAAATTTGACAAATGGGAGAAAGCTTATCCAGC 374
Db      301 AGACTCTACGAGGAGCGAGCTGGGAAATTTGACAAATGGGAGAAAGCTTATCCAGC 360
QY      375 CATGCCGCTGTGTGAAGAGGCTTCGATTTGTAAGCACTTTAGTTGGAGAGAGG 434
Db      361 CATGCCGCTGTGTGAAGAGGCTTCGATTTGTAAGCACTTTAGTTGGAGAGAGG 420
QY      435 TTGTAGATTAACTCTGCAATTTGAGCTTACCGACAGATTAAGCACTGCTACTG 494
Db      421 CATTAACCTAATACGTTAGTGTGTAAGTTGAGGTTACGACAGATTAAGCACTGCT 480
QY      495 TGCAGACAGCCCGGTAATACAGAGGAGTCAAGGCTTATCGAAATTAAGTGGCGTAA 554
Db      481 TGCAGACAGCCCGGTAATACAGAGGAGTCAAGGCTTATCGAAATTAAGTGGCGTAA 540
QY      555 CGCGGTAGGTGTTGTTAAGTTGATGTAAGTTCCCGGGCTCAACTGGGAACTGCA 614
Db      541 CGCGGTAGGTGTTGTTAAGTTGATGTAAGTTCCCGGGCTCAACTGGGAACTGCA 600
QY      615 TTCAAACTGACTGACTAGATGATGAGGAGTGGAGAAATTTCCGTGTACGGTGA 674
Db      601 TTCAAACTGACTGACTAGATGATGAGGAGTGGAGAAATTTCCGTGTACGGTGA 660
QY      675 ATGCGTATATAGGAGGAAACACCAAGTGGGAGGAGGACCACTGAGCTAATAC 734
Db      661 ATGCGTATATAGGAGGAAACACCAAGTGGGAGGAGGACCACTGAGCTAATAC 720
QY      735 CTGAGGTGCGAAAGGCTGGGAGGAGCAACAGATTAAGTACCCTGTGTACAGCGCTAA 794
Db      721 CTGAGGTGCGAAAGGCTGGGAGGAGCAACAGATTAAGTACCCTGTGTACAGCGCTAA 780
QY      795 ACGATGTCAACTAGCCGTTGGAAGCTTGAAGCTTTAGTGGCGAGCTAACGATTAAGT 854
Db      781 ACGATGTCAACTAGCCGTTGGAAGCTTGAAGCTTTAGTGGCGAGCTAACGATTAAGT 840
QY      855 TGCAGCGCTGGGAGTACGCGCCGCAAGGTTAAACTCAATGAATGAACGCGGGCCCGCA 914
Db      841 TGCAGCGCTGGGAGTACGCGCCGCAAGGTTAAACTCAATGAATGAACGCGGGCCCGCA 900
QY      915 CAAGCGGTGAGCAATGTGTTAATTTGAGAGCAACGAGAAACCTTACAGGCTTGAC 974
Db      901 CAAGCGGTGAGCAATGTGTTAATTTGAGAGCAACGAGAAACCTTACAGGCTTGAC 960
QY      975 ATCCAAATGAATCTTTCTAGAGATAGATGTGTCCTTGGGAAACATTGAGACAGGTCTGA 1034
Db      961 ATCCAAATGAATCTTTCTAGAGATAGATGTGTCCTTGGGAAACATTGAGACAGGTCTGA 1020
QY      1035 TGGCTGTGTCAGCTGCTGTGTGAATGTAAAG 1068
Db      1021 TGGCTGTGTCAGCTGCTGTGTGAATGTAAAG 1054

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RESULT 11
 US-09-791-610-1
 ; Sequence 1, Application US/09791610
 ; Publication No. US20030100084A1
 ; GENERAL INFORMATION:

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; APPLICANT: Canon Inc.
; TITLE OF INVENTION: Polyhydroxyalkanoate containing 3-hydroxybenzoylelkanic acid
; TITLE OF INVENTION: monomer unit, and method for producing the same.
; FILE REFERENCE: 4396021
; CURRENT APPLICATION NUMBER: US/09/791,610
; CURRENT FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 1
; SEQ ID NO: 1
; TYPE: DNA
; LENGTH: 1501
; ORGANISM: Pseudomonas jessenii 161 strain.
; US-09-791-610-1

Query Match      92.1%; Score 985.2; DB 11; Length 1501;
Best Local Similarity 95.9%; Pred. No. 1.3e-292;
Matches 1011; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY      15 TGAACGCTGCGGAGCGCTTACACATGCAAGTCGAGCGGTAGAGAGAAAGCTTGCTTC 74
Db      1 TGAACGCTGCGGAGCGCTTACACATGCAAGTCGAGCGGTAGAGAGAAAGCTTGCTTC 60
QY      75 TTGAGAGCGGCGGACGGGTGATATGCTTACGAAATCTGCTGTGTGTGGGATTAAGT 134
Db      61 AATTGAGCGGAGCGGAGTATGCTTACGAAATCTGCTGTGTGTGGGATTAAGT 120
QY      135 TCGAAAACGGACGCTAATACCGCATACGCTTACGGGAGAAAGAGGAGACCTTCGGGCC 194
Db      121 CTCGAAAGGAGCGCTAATACCGCATACGCTTACGGGAGAAAGAGGAGACCTTCGGGCC 180
QY      195 TTGGCGCTACAGATGAGCGCTAGTGGATTAAGTGTGTAAGTATGCTTACCAAG 254
Db      181 TTGGCGCTACAGATGAGCGCTAGTGGATTAAGTGTGTAAGTATGCTTACCAAG 240
QY      255 GCGAGCATCCGTAACCTGCTGAGAGATGATCAGTCAAGTGAACCTGAGACAGCTCC 314
Db      241 GCGAGCATCCGTAACCTGCTGAGAGATGATCAGTCAAGTGAACCTGAGACAGCTCC 300
QY      315 TTGCGGTATCAGATGAGCGCTAGTGGATTAAGTGTGTAAGTATGCTTACCAAG 374
Db      301 TTGCGGTATCAGATGAGCGCTAGTGGATTAAGTGTGTAAGTATGCTTACCAAG 360
QY      375 CATGCCGCTGTGTGAAGAGGCTTCGATTTGTAAGCACTTTAGTTGGAGAGAGG 434
Db      361 CATGCCGCTGTGTGAAGAGGCTTCGATTTGTAAGCACTTTAGTTGGAGAGAGG 420
QY      435 TTGTAGATTAACTCTGCAATTTGAGCTTACCGACAGATTAAGCACTGCTACTG 494
Db      421 CATTAACCTAATACGTTAGTGTGTAAGTTGAGGTTACGACAGATTAAGCACTGCT 480
QY      495 TGCAGACAGCCCGGTAATACAGAGGAGTCAAGGCTTATCGAAATTAAGTGGCGTAA 554
Db      481 TGCAGACAGCCCGGTAATACAGAGGAGTCAAGGCTTATCGAAATTAAGTGGCGTAA 540
QY      555 CGCGGTAGGTGTTGTTAAGTTGATGTAAGTTCGAGGCTAACCTGCGGAACTGCA 614
Db      541 CGCGGTAGGTGTTGTTAAGTTGATGTAAGTTCGAGGCTAACCTGCGGAACTGCA 600
QY      615 TTCAAACTGACTGACTAGATGATGAGGAGTGGAGAAATTTCCGTGTACGGTGA 674
Db      601 TTCAAACTGACTGACTAGATGATGAGGAGTGGAGAAATTTCCGTGTACGGTGA 660
QY      675 ATGCGTATATAGGAGGAAACACCAAGTGGGAGGAGGACCACTGAGCTAATAC 734
Db      661 ATGCGTATATAGGAGGAAACACCAAGTGGGAGGAGGACCACTGAGCTAATAC 720
QY      735 CTGAGGTGCGAAAGGCTGGGAGGAGCAACAGATTAAGTACCCTGTGTACAGCGCTGA 794
Db      721 CTGAGGTGCGAAAGGCTGGGAGGAGCAACAGATTAAGTACCCTGTGTACAGCGCTGA 780
QY      795 ACGATGTCAACTAGCCGTTGGAAGCTTGAAGCTTTAGTGGCGAGCTAACGATTAAGT 854
Db      781 ACGATGTCAACTAGCCGTTGGAAGCTTGAAGCTTTAGTGGCGAGCTAACGATTAAGT 840

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Db 841 TGACCCCTCGGGAGTAGACGGCCGCAGASGTTAAATCTAAATGAATTAGACGGGGGCCCGCA 900

QY 915 CAAGCGGTGAGCATGTGGTTTAATTCGAGCAACGCGAAACCTTTACAGGCTTTGAC 974

Db 901 CAAGCGGTGAGCATGTGGTTTAATTCGAGCAACGCGAAACCTTTACAGGCTTTGAC 960

QY 975 ATTCATGAACTTTCTAAGATAGATTGGTCCCTTCGGGAACATTGAGCAGGTGTGCA 1034

Db 961 ATTCATGAACTTTCTAAGATAGATTGGTCCCTTCGGGAACATTGAGCAGGTGTGCA 1020

QY 1035 TGAGCTGTCAGCTGCTGTTGTGAATGTAAAG 1068

Db 1021 TGAGCTGTCAGCTGCTGTTGTGAATGTAAAG 1054

```

RESULT 9
US-09-793-920A-1
; Sequence 1, Application US/09793920A
; Patent No. US2002006589A1
; GENERAL INFORMATION:
; APPLICANT: Canon Inc.
; TITLE OF INVENTION: Polyhydroxyalkanoate containing 3-hydroxyphenylalkanoic acid as
; TITLE OF INVENTION: comonomer unit, and method for producing the same.
; FILE REFERENCE: 4396021
; CURRENT APPLICATION NUMBER: US/09/793,920A
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 1
; SEQ ID NO 1
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii 161 strain.
US-09-793-920A-1

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Query Match	92.1%;	Score 985.2;	DB 9;	Length 1501;
Best Local Similarity	95.9%;	Pred. No. 1.3e-292;		
Matches 101;	Conservative	0;	Mismatches 43;	Indels 0;
				Gaps 0;

QY	1	TTGAACGCTGGCGGACAGCCCTTAACACATATGCAAGTCGAGCGGTGAAGAAAGCTTCCTC	74
Db	1	TGAACGCTGGCGGACAGCCCTTAACACATATGCAAGTCGAGCGGTGAAGAAAGCTTCCTC	60
QY	75	TTGAGAGCGGCGGACCGGTGATGATGCTCTAGGAATCTGCTGTATGTGGGGATTAACGT	134
Db	61	AATTCAGCGCGCGGACCGGTGATGATGCTCTAGGAATCTGCTGTATGTGGGGATTAACGT	120
QY	135	TCGGAAACGGAGCCTAATACCGCATTCGCTCAACGGAGAAAGCAAGGGGACCTTCGGGCGC	194
Db	121	CTCGAAGGGAACCTTAATACCGCATTCGCTCAACGGAGAAAGCAAGGGGACCTTCGGGCGC	180
QY	195	TTGGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTAGGGTAATGGCTCAACAG	254
Db	181	TTGGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTAGGGTAATGGCTCAACAG	240
QY	255	GCGACCATCCGCTAATCTGCTGAGAGAGATGATCAATGCACATCGAATCTGAAACACGGCTC	314
Db	241	GCGACCATCCGCTAATCTGCTGAGAGAGATGATGATGCACATCGAATCTGAAACACGGCTC	300
QY	315	AGACTCCTACGGGAGGACAGTAGTGGGAATATTGACAAATGGGCGAAACCTGATCCAGC	374
Db	301	AGACTCCTACGGGAGGACAGTAGTGGGAATATTGACAAATGGGCGAAACCTGATCCAGC	360
QY	375	CATGCCCGCGTCTGAAAGAAAGCTTCGGATTGTAAACACTTAAAGTTGGAGAGAAAGG	433
Db	361	CATGCCCGCGTCTGAAAGAAAGCTTCGGATTGTAAAGCACTTAAAGTTGGAGAGAAAGG	420
QY	435	TTGTAGATTATACTGTGCAATTTGACGTTACCGACGAATTAAGCACCGCTAATCTG	494
Db	421	CATTAACTTAATCGTTAGTGTGTTTGAAGCTTACCGACGAATTAAGCACCGCTAATCTG	480
QY	495	TTCGACAGACCGCGGTAAATCAGAGGCTCAACGCTTAATCGAATTATCTGGCGTTAAG	554
Db	481	TTCGACAGACCGCGGTAAATCAGAGGCTCAACGCTTAATCGAATTATCTGGCGTTAAG	540

QY	555	CGCGCGTAGCTGTTTGGTAAAGTTGAATGGAATCCCCGGGCTCAACTGGGAATCTGA	614
Db	541	CGCGCGTAGCTGTTTGGTAAAGTTGAATGGAATCCCCGGGCTCAACTGGGAATCTGA	600
QY	615	TTCAAAACTGACTGACTAGATATGTAGAGGGTGGTGAATTTCTGTGTAGCGGTAA	674
Db	601	TTCAAAACTGACTGACTAGATATGTAGAGGGTGGTGAATTTCTGTGTAGCGGTAA	660
QY	675	ATGCGTAGTATAGGAAGAAACACAGTAGCGGAAGCGAACACACTGATTAATACAGCA	734
Db	661	ATGCGTAGTATAGGAAGAAACACAGTAGCGGAAGCGAACACACTGATTAATACAGCA	720
QY	735	CTGAGGTGCGAAGCGTGGGAGCGAAACAGAAATTAGTAACTCTGTAGTCCACGCGTAA	794
Db	721	CTGAGGTGCGAAGCGTGGGAGCGAAACAGAAATTAGTAACTCTGTAGTCCACGCGTAA	780
QY	795	ACGAGTCAACATGACCGCTTGAAGCCTTGAGCTTTTAGTAGGGGCGACGTACGCACTTAAGT	854
Db	781	ACGAGTCAACATGACCGCTTGAAGCCTTGAGCCTTTAGTAGGGGCGACGTACGCACTTAAGT	840
QY	855	TGACCGCCTGGGGAGTACGCGCGCAAGGTTAAACTCCAATGATTAATGACGGGGGCGCGCA	914
Db	841	TGACCGCCTGGGGAGTACGCGCGCAAGGTTAAACTCCAATGATTAATGACGGGGGCGCGCA	900
QY	915	CAAGCGGTGAGCAATGTGCTTTAATTGGAAGCAACCGAAGAACCTTACACAGSCTTAC	974
Db	901	CAAGCGGTGAGCAATGTGCTTTAATTGGAAGCAACCGAAGAACCTTACACAGSCTTAC	960
QY	975	ATCCATATGAATTTTAAAGATAGATTGTGGCTTCGGGAAACATTGAGACAGAGCTCTCA	1034
Db	961	ATCCATATGAATTTTCAAGATGATGGGTGCTTCGGGAAACATTGAGACAGAGCTCTCA	1020
QY	1035	TGGCTGTCTCAAGCTCGCTGTTGTGAATATGMAAG	1068
Db	1021	TGGCTGTCTCAAGCTCGCTGTTGTGAATATGTTGAG	1054

```

RESULT 10
US-09-951-720-1
; Sequence 1, Application US/09551720
; Patent No. US20020160467A1
; GENERAL INFORMATION:
; APPLICANT: Caron Kabushiki Kaisha
; TITLE OF INVENTION: Polyhydroxyalkanoate and Manufacturing Method Thereof
; FILE REFERENCE: 4477001
; CURRENT APPLICATION NUMBER: US/09/951,720
; CURRENT FILING DATE: 2000-09-14
; PRIORITY APPLICATION NUMBER: JP 279900/2000
; JP 378827/2000
; JP 168238/2001
; JP 168509/2001
; JP 275063/2001
; PRIORITY FILING DATE: 2000-09-14
; 2000-12-13
; 2001-05-31
; 2001-05-31
; 2001-09-11
; NUMBER OF SEQ ID NOS: 1
; SEQ ID NO 1
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii P1c1 strain.
US-09-951-720-1

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	Query Match	92.1%;	Score 985.2;	DB 10;	Length 1501;
	Best Local Similarity	95.1%;	Pred. No. 1.3e-292;		
	Matches 1011;	Conservative	0;	Mismatches 43;	Indels 0;
				Gaps	0;
Oy	15	TCAGCGCTGGCGGAGCGCTTACACAGCGAAGTCGAGCGGTGAGAGAACTTGCTTCTC			74
Db	1	TGAGCCCTGAGCGCGAGCGCTTACACATGACAGTGGAGCGGATGACCGAGACTTGCTCTCG			60
Oy	75	TTGAGAGCGGCGGAGCGGAGTGAATGCTGCTGGTATGGGAGGATACGT			134

QY 795 ACGATGTCAACTACCGCTTGGAAAGCCTTGAAGCTTTTATGTCGCGACGCTAACGCACTTAAGT 854
DB 781 ACGATGTCAACTACCGCTTGGAAAGCCTTGAAGCTTTTATGTCGCGACGCTAACGCACTTAAGT 840
QY 855 TGACCGCTGCGGAGAGTACCGCGCGCAAGGTTAAACCAATGAATTTAGCGGGGCGCCGCA 914
DB 841 TGACCGCTGCGGAGAGTACCGCGCGCAAGGTTAAACCAATGAATTTAGCGGGGCGCCGCA 900
QY 915 CAAGCGGTGAGCATGTGTTTAAATTCGAAGCAACGCGAAGAACTTACCAAGCCTTAC 974
DB 901 CAAGCGGTGAGCATGTGTTTAAATTCGAAGCAACGCGAAGAACTTACCAAGCCTTAC 960
QY 975 ATCCAAATGAACCTTTAGAGATAGATTTGGTCCCTTGGGAAACATTTGAGACAGCTGTCA 1034
DB 961 ATCCAAATGAACCTTTAGAGATAGATTTGGTCCCTTGGGAAACATTTGAGACAGCTGTCA 1020
QY 1035 TGCGTGTCTGACGCTGCTGTTTGAATGTAAG 1068
DB 1021 TGCGTGTCTGACGCTGCTGTTGTAATGTTGG 1054

RESULT 6

US-09-745-476-1
; Sequence 1, Application US/09745476
; Patent No. US20010029039A1
; GENERAL INFORMATION:
; APPLICANT: CANON INC.
; TITLE OF INVENTION: Preparation of Poly-hydroxyalkanoic Acid
; FILE REFERENCE: 4351008
; CURRENT APPLICATION NUMBER: US/09/745,476
; CURRENT FILING DATE: 2000-12-26
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Microsoft Word
; SEQ ID NO: 1
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii P161 ; FERM P-17445
US-09-745-476-1

Query Match 92.1%; Score 985.2; DB 9; Length 1501;
Best Local Similarity 95.9%; Pred. No. 1.3e-292;
Matches 1011; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 15 TGAACGCTGCGGCGGAGCCTTAACATGCAAGTCGACGCGTGAAGAGAAAGCTTCTTC 74
DB 1 TGAACGCTGCGGCGGAGCCTTAACATGCAAGTCGACGCGTGAAGAGAAAGCTTCTTC 60
QY 75 TTGAGAGCGGCGGAGCGGTGAGTAATGCTTAGGAATCTGCTGTAAGTGGGGATTAAGT 134
DB 61 AATTCAAGCGGCGGAGCGGTGAGTAATGCTTAGGAATCTGCTGTAAGTGGGGATTAAGT 120
QY 135 TCGAAAACGAGCCTAATACCGCATACGCTCTACGCGGAAAGCAAGGGAACCTTCGCGCC 194
DB 121 CTCGAAAGGAGCCTAATACCGCATACGCTCTACGCGGAAAGCAAGGGAACCTTCGCGCC 180
QY 195 TTGCGCTATGAGTACGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 254
DB 181 TTGCGCTATGAGTACGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 240
QY 255 GCGACGATCCGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 314
DB 241 GCGACGATCCGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
QY 315 AGACTCTTACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 374
DB 301 AGACTCTTACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
QY 375 CATGCCGCTGTGTGAAGAAGGCTTCGATTTGAAGCACTTAAGTTGGAGGAGGAGG 434
DB 361 CATGCCGCTGTGTGAAGAAGGCTTCGATTTGAAGCACTTAAGTTGGAGGAGGAGG 420
QY 435 TTGTAGATTAAATCTCTGCAATTTTGAAGTTACCGACAGATTAAGCAACCGGCTAACTCTG 494

DB 421 CATTAACCTAATACCTTATGTTTGTGACCTTAACGACAAATGAAGCAACCGGCTAACTCTG 480
QY 495 TGCCACACACCGCGGTAATACAGAGGTGCAAGCCTTAATGCAATTAAGTGGGCGTAAG 554
DB 481 TGCCACACACCGCGGTAATACAGAGGTGCAAGCCTTAATGCAATTAAGTGGGCGTAAG 540
QY 555 CCGCGCTAGCTGTTTGTTAAGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 614
DB 541 CCGCGCTAGCTGTTTGTTAAGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
QY 615 TTCAAACTGCACTGATAGATAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 674
DB 601 TTCAAACTGCACTGATAGATAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 675 ATCCGTAATATAGAGAGAACACGATGCGGAAAGGCGACCACTTGAATATGACA 734
DB 661 ATCCGTAATATAGAGAGAACACGATGCGGAAAGGCGACCACTTGAATATGACA 720
QY 735 CTGAGGTGGAAGAGGTGGGAGCAACAGGATTAGATACCTGATGATGATGATGATGATGAT 794
DB 721 CTGAGGTGGAAGAGGTGGGAGCAACAGGATTAGATACCTGATGATGATGATGATGATGAT 780
QY 795 ACGATGTCAACTACCGCTTGGAAAGCCTTGAAGCTTTTATGTCGCGACGCTAACGCACTTAAGT 854
DB 781 ACGATGTCAACTACCGCTTGGAAAGCCTTGAAGCTTTTATGTCGCGACGCTAACGCACTTAAGT 840
QY 855 TGACCGCTGCGGAGAGTACCGCGCGCAAGGTTAAACCAATGAATTTAGCGGGGCGCCGCA 914
DB 841 TGACCGCTGCGGAGAGTACCGCGCGCAAGGTTAAACCAATGAATTTAGCGGGGCGCCGCA 900
QY 915 CAAGCGGTGAGCATGTGTTTAAATTCGAAGCAACGCGAAGAACTTACCAAGCCTTAC 974
DB 901 CAAGCGGTGAGCATGTGTTTAAATTCGAAGCAACGCGAAGAACTTACCAAGCCTTAC 960
QY 975 ATCCAAATGAACCTTTAGAGATAGATTTGGTCCCTTGGGAAACATTTGAGACAGCTGTCA 1034
DB 961 ATCCAAATGAACCTTTAGAGATAGATTTGGTCCCTTGGGAAACATTTGAGACAGCTGTCA 1020
QY 1035 TGCGTGTCTGACGCTGCTGTTTGAATGTAAG 1068
DB 1021 TGCGTGTCTGACGCTGCTGTTGTAATGTTGG 1054

RESULT 7

US-09-821-016-5
; Sequence 5, Application US/09821016
; Patent No. US2001004692A1
; GENERAL INFORMATION:
; APPLICANT: CANON INC.
; TITLE OF INVENTION: Polyhydroxyalkanoate Synthase and Gene Encoding the Same Enzym
; FILE REFERENCE: 4051021
; CURRENT APPLICATION NUMBER: US/09/821,016
; CURRENT FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Microsoft Word
; SEQ ID NO: 5
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii P161 ; BP-7376
US-09-821-016-5

Query Match 92.1%; Score 985.2; DB 9; Length 1501;
Best Local Similarity 95.9%; Pred. No. 1.3e-292;
Matches 1011; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 15 TGAACGCTGCGGCGGAGCCTTAACATGCAAGTCGACGCGTGAAGAGAAAGCTTCTTC 74
DB 1 TGAACGCTGCGGCGGAGCCTTAACATGCAAGTCGACGCGTGAAGAGAAAGCTTCTTC 60
QY 75 TTGAGAGCGGCGGAGCGGTGAGTAATGCTTAGGAATCTGCTGTAAGTGGGGATTAAGT 134
DB 61 AATTCAAGCGGCGGAGCGGTGAGTAATGCTTAGGAATCTGCTGTAAGTGGGGATTAAGT 120

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Db      1 TCGAGCGGTAGAGAGAGCTTGCTTCTCTTGAGACGGCGGACGGGTAGATATGCTTAG 60
Qy      107 GAATCTGCTCGGTAGTGTGGGAGATTAAGTTGGAAACGACGCTAATACCGATACGTCT 166
Db      61 GAATCTGCTCGGTAGTGTGGGAGATTAAGTTGGAAACGACGCTAATACCGATACGTCT 120
Qy      167 ACCGAGAAAAGCAGGAGACCTTGGGCTTGGCTATCAGATGACCTAGGTGGATTAG 226
Db      121 ACCGAGAAAAGCAGGAGACCTTGGGCTTGGCTATCAGATGACCTAGGTGGATTAG 180
Qy      227 CTGTGTGTGAGGTAAATGCTCAACAGGCGACATCCGTTAATCTGCTTGAAGATGAT 286
Db      181 CTGTGTGTGAGGTAAATGCTCAACAGGCGACATCCGTTAATCTGCTTGAAGATGAT 240
Qy      287 CAGTCACTGTAATCTGAGACACGCTCAGATCCCTTACGGGAGGACAGGAGGAAATAT 346
Db      241 CAGTCACTGTAATCTGAGACACGCTCAGATCCCTTACGGGAGGACAGGAGGAAATAT 300
Qy      347 TGGACAAATGGGCGAAGCCTGATCCAGCCATGCCGCTGTGTGAAGAGTCTTGGATT 406
Db      301 TGGACAAATGGGCGAAGCCTGATCCAGCCATGCCGCTGTGTGAAGAGTCTTGGATT 360
Qy      407 GTAAGCACTTAAGTTGGAGAGAGGCTGTGATTAATATCTGCAATTTTGAAGTTA 466
Db      361 GTAAGCACTTAAGTTGGAGAGAGGCTGTGATTAATATCTGCAATTTTGAAGTTA 420
Qy      467 CCGACAGAAATAGCACCGGCTAATCTGTGACAGACGCGGTTAATACAGAGGTTCAA 526
Db      421 CCGACAGAAATAGCACCGGCTAATCTGTGACAGACGCGGTTAATACAGAGGTTCAA 480
Qy      527 GCGTTATCGGAAATTAATGCGGCTAAAGCGGCGATAGTGTGTTTAACTGATGTA 586
Db      481 GCGTTATCGGAAATTAATGCGGCTAAAGCGGCGATAGTGTGTTTAACTGATGTA 540
Qy      587 AATCCCGGAGCTCAACCTGAGGAACTGCAATTCATACTGATGATAGTATGATAGG 646
Db      541 AATCCCGGAGCTCAACCTGAGGAACTGCAATTCATACTGATGATAGTATGATAGG 600
Qy      647 GTGTGTGAATTTCTGTGTGAGCGGTGAATGTGTGATATAGAAAGAACCAAGTGG 706
Db      601 GTGTGTGAATTTCTGTGTGAGCGGTGAATGTGTGATATAGAAAGAACCAAGTGG 660
Qy      707 AAGGCGACCACTGAGCTAATACTGACATGAGGTGCAAAAGCGTGGGAGCAACAGA 766
Db      661 AAGGCGACCACTGAGCTAATACTGACATGAGGTGCAAAAGCGTGGGAGCAACAGA 720
Qy      767 TTGATACCTCTGTGTGATCCAGCGCTTAACGATGCACTAGCGTTGGAAGCTTTAG 826
Db      721 TTGATACCTCTGTGTGATCCAGCGCTTAACGATGCACTAGCGTTGGAAGCTTTAG 780
Qy      827 TTTTATGCGCAGCTTAACGCAATTAAGTTGACCGGCTGGGAGTACGGCGCAGTTAA 886
Db      781 TCTTATGCGCAGCTTAACGCAATTAAGTTGACCGGCTGGGAGTACGGCGCAGTTAA 840
Qy      887 AACTCAAATGAATTGACGGGCGCCGCAACAGCGGTGAGCATGTGTTTAAATCGAAG 946
Db      841 AACTCAAATGAATTGACGGGCGCCGCAACAGCGGTGAGCATGTGTTTAAATCGAAG 900
Qy      947 AACGGAAGACCTTACCAAGGCTTGAATCCATGAATCTTACAGATATGATTGTGC 1006
Db      901 AACGGAAGACCTTACCAAGGCTTGAATCCATGAATCTTACAGATATGATTGTGC 960
Qy      1007 CTTTGGGAACATTGAGACAGGTGTGCAATGCTGTGCTCACTGTGTGAAATGTA 1066
Db      961 CTTTGGGAACATTGAGACAGGTGTGCAATGCTGTGCTCACTGTGTGAAATGTA 1020
Qy      1067 GG 1068
Db      1021 GG 1022
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RESULT 5

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US-09-791-592-1
; Sequence 1: Application US/09791592
; Patent No. US20010021223A1
; GENERAL INFORMATION:
; APPLICANT: Canon Inc.
; TITLE OF INVENTION: Polymethacrylate containing 3-hydroxybenzoic acid
; FILE REFERENCE: 4396021
; CURRENT APPLICATION NUMBER: US/09/791,592
; NUMBER OF SEQ ID NOS: 1
; SEQ ID NO 1
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jesseni 161 strain.
US-09-791-592-1
Query Match 92.1%; Score 985.2; DB 9; Length 1501;
Best Local Similarity 95.9%; Pred. No. 1.3e-292;
Matches 1011; Conservative 0; Mismatches 43; Indels 0; Gaps 0;
Qy      15 TGAAGCTGCGGCGGAGGCTTAACATGCAAGTGCAGGTAGAGAAAGCTTGTCTC 74
Db      1 TGAAGCTGCGGCGGAGGCTTAACATGCAAGTGCAGGTAGAGAAAGCTTGTCTC 60
Qy      75 TTGAGAGCGGCGGAGGCTGATATGCTTGAATCTGCTGTGTGAGTATGCTTGAAGT 134
Db      61 AATTGAGCGGCGGAGGCTGATATGCTTGAATCTGCTGTGTGAGTATGCTTGAAGT 120
Qy      135 TCGGAAAGGAGCGGCTAATACCGCATACGCTCTAGGAGAGGAGGAGGAGGCTTGG 194
Db      121 CTGGAAGGAGCGGCTAATACCGCATACGCTCTAGGAGAGGAGGAGGAGGCTTGG 180
Qy      195 TTGCGCTATCAGATGAGGCTTGAATGCTGATGATGATGATGATGATGATGATGAT 254
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Db      241 GCGAGATCGGCTAATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 300
Qy      315 AGACTCTTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 374
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Qy      495 TGCAGAGCGGCGGCTAATACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 554
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Qy      555 GCGCGTGTGAGGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 614
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Db      601 TTCAAACCTGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
Qy      675 ATGCGTATGATTAAGAGAGAACCACTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 734
Db      661 ATGCGTATGATTAAGAGAGAACCACTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
Qy      735 CTGAGGTGCGAAGCGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 794
Db      721 CTGAGGTGCGAAGCGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
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DB 911 CGGGGGCCCGCACAAAGCGGTGAGCATGTGTTTAATTCGAAGCAACCGGAAGAACTTTA 970
QY 963 CGAGCCTTGAATCCAAATGAATTTCTGAGATAGATTTGGCTTCGGGAACATTTAG 1022
DB 971 CGAGCCTTGAATCCAAATGAATTTCTGAGATAGATTTGGCTTCGGGAACATTTAG 1030
QY 1023 ACAGGTGCTGATGCTGTGCTGAGCTGCTGTGTTGTAATGTAAG 1068
DB 1031 ACAGGTGCTGATGCTGTGCTGAGCTGCTGTGTTGTAATGTAAG 1076

RESULT 3
US-10-007-527A-12
Sequence 12, Application US/10007527A
Publication No. US20030044807A1
GENERAL INFORMATION:
APPLICANT: Tomb, Jean-Francois
APPLICANT: Bramucci, Michael G.
APPLICANT: Cheng, Qiong
APPLICANT: Kostichka, Kristy N.
TITLE OF INVENTION: Rhodococcus Cloning and Expression Vectors
CURRENT APPLICATION NUMBER: US/10/007,527A
PRIOR FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 60/254,868
PRIOR FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Microsoft Office 97
SEQ ID NO 12
LENGTH: 1424
TYPE: DNA
ORGANISM: Rhodococcus AN12
US-10-007-527A-12

Query Match 92.5%; Score 990; DB 15; Length 1424;
Best Local Similarity 98.0%; Pred. No. 4.1e-294;
Matches 1002; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 47 TCAGCGCTAGAGAGAGCTTCTCTTCTGAGAGCGGAGCGGTGATGCTAG 106
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QY 107 GAATCTGCTGTAGTGGGAGATAGCTTCGAAAGCGAGCTTAATACCGCATAGCTCT 166
DB 61 GAATCTGCTGTAGTGGGAGATAGCTTCGAAAGCGAGCTTAATACCGCATAGCTCT 120
QY 167 ACGGAGAAAGCAGGGAGACTTGGGCTTGGCTTTCAGATGAGCTTAGTGGATTAG 226
DB 121 ACGGAGAAAGCAGGGAGACTTGGGCTTGGCTTTCAGATGAGCTTAGTGGATTAG 180
QY 227 CTAGTTGATGAGTAAATGCTCAACAGGCGAGCATCCCTAATCTGCTGAGAGATGAT 286
DB 181 CTAGTTGATGAGTAAATGCTCAACAGGCGAGCATCCCTAATCTGCTGAGAGATGAT 240
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DB 241 CAGTCACACTGGAACCTGAGACAGGTCCAGACTTCTTAACGGAGCGCAGCTGGGAAAT 300
QY 347 TGGACATGGGCGAAAGCTGATCCAGCCATGCGGCTGTGAGAAAGCTTTGCGATT 406
DB 301 TGGACATGGGCGAAAGCTGATCCAGCCATGCGGCTGTGAGAAAGCTTTGCGATT 360
QY 407 GTAAAGCACTTTAAGTTGGAGAGAGGTTGATTAATCTCTGCAATTTTGAAGTTA 466
DB 361 GTAAAGCACTTTAAGTTGGAGAGAGGTTGATTAATCTCTGCAATTTTGAAGTTA 420

QY 467 CCGACAGAAATTAAGACCCGGCTACTCTGAGCAGAGCCGGGTAAATACAGAGGATGCA 526
DB 421 CCGACAGAAATTAAGACCCGGCTACTCTGAGCAGAGCCGGGTAAATACAGAGGATGCA 480
QY 527 GCGTTAATCGAATTAATGAGCGGTAAAGCGCGGTAGTGTGTTTGAATTGATGTA 586
DB 481 GCGTTAATCGAATTAATGAGCGGTAAAGCGCGGTAGTGTGTTTGAATTGATGTA 540
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DB 541 AATCCCGGAGCTCAACCTGGGAGATGCAATCAATCAATCTGATGATGATGAG 600
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DB 721 TTGATATACCTGCTGATGCTCCAGCCGCTAAACGATGCACTAGCCGTTGAAAGCTTGA 780
QY 827 TTTTATGCGCGAGCTTAAGCATTAAGTTGACCGCTTGGGAGTACCGCCGCAAGTTAA 886
DB 781 TTTTATGCGCGAGCTTAAGCATTAAGTTGACCGCTTGGGAGTACCGCCGCAAGTTAA 840
QY 887 AACTCAATGAATTAAGAGCGGCGCGCAACAGCGGTGAGATGTTTAAATGCAAGC 946
DB 841 AACTCAATGAATTAAGAGCGGCGCGCAACAGCGGTGAGATGTTTAAATGCAAGC 900
QY 947 AACGCAAGAACCTTAACAGGCTTGAATCAATCAATCTTCTAGACATGATTTGTC 1006
DB 901 AACGCAAGAACCTTAACAGGCTTGAATCAATCAATCTTCTAGACATGATTTGTC 960
QY 1007 CTTGCGGAAATTTGAGACAGGTGCTGATGCTGCGACGCTGTTGTAATGTA 1066
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QY 1067 GG 1068
DB 1021 GG 1022

RESULT 4
US-10-007-452-12
Sequence 12, Application US/10007452
Publication No. US20030093701A1
GENERAL INFORMATION:
APPLICANT: Tomb, Jean-Francois
APPLICANT: Bramucci, Michael G.
APPLICANT: Cheng, Qiong
APPLICANT: Kostichka, Kristy N.
TITLE OF INVENTION: Rhodococcus Cloning and Expression Vectors
CURRENT APPLICATION NUMBER: US/10/007,452
PRIOR FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: 60/254,868
PRIOR FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Microsoft Office 97
SEQ ID NO 12
LENGTH: 1424
TYPE: DNA
ORGANISM: Rhodococcus AN12
US-10-007-452-12

Query Match 92.5%; Score 990; DB 15; Length 1424;
Best Local Similarity 98.0%; Pred. No. 4.1e-294;
Matches 1002; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 47 TCAGCGCTAGAGAGAGCTTCTCTTCTGAGAGCGGAGCGGTGATGCTAG 106

Db 121 GTGGGGGATTAAGCTTGGAAACGACGCTAATACCGCATACGCTCTACGGAGAAACAG 180
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 QY 301 CTGAGACAGGCTCCAGACTCTTAAGGAGGAGCGAGCGAGGAGATATTGGACAAGGCGCA 360
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 QY 361 AAGCTGATCCAGCCATGCGCGGTGTGTGAAGAGGTCTTCGATTGTAAGCATTTAA 420
 Db 361 AAGCTGATCCAGCCATGCGCGGTGTGTGAAGAGGTCTTCGATTGTAAGCATTTAA 420
 QY 421 GTTGGGAGGAGGGTGTGATTAATACCTGCGAATTTTGAAGTTACCGACAGATAAGC 480
 Db 421 GTTGGGAGGAGGGTGTGATTAATACCTGCGAATTTTGAAGTTACCGACAGATAAGC 480
 QY 481 ACCGGCTAACTCTGTGCGACGACCGCGGTAAATACAGAGGGTGCAGCGTTAATCGGAAT 540
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 QY 541 TACTGGGCTTAAGGGCGGTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
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 QY 601 ACCCTGGAACTGCTATTCATAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 660
 Db 601 ACCCTGGAACTGCTATTCATAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 660
 QY 661 TGTGTAGCGGTAAATGCGT 720
 Db 661 TGTGTAGCGGTAAATGCGT 720
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 Db 721 GACTAATCTGACATGAGGTGCGAAGCGTGGGAGCAACAGATTAGTATCCCTGTGT 780
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RESULT 2

US-09-737-297-5

Sequence 5, Application US/09737297

Patent No. US2002072108A1

GENERAL INFORMATION:

APPLICANT: Berry, Mark

APPLICANT: Griffiths, Allen

APPLICANT: Hill, Philip

APPLICANT: Laybourne-Parry, Johanna

APPLICANT: Mills, Sarah

; TITLE OF INVENTION: Processes and Organisms for the Production of Antifreeze Proti
 ; FILE REFERENCE: F3347
 ; CURRENT APPLICATION NUMBER: US/09/737,297
 ; PRIOR FILING DATE: 2000-12-15
 ; PRIOR APPLICATION NUMBER: GB 9929696.4
 ; PRIOR FILING DATE: 1999-12-15
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 5
 ; LENGTH: 1140
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas syzyxantha
 ; US-09-737-297-5

Query Match 98.7%; Score 1056.4; DB 9; Length 1140;
 Best Local Similarity 99.4%; Pred. No. 1.8e-314;
 Matches 1060; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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 Db 551 CTGGGCGTAAAGCGCGGT 610
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 QY 663 TGTAGCGGTAAATGCGTAAATTAAGAAAGAAACACAGATGCGGAAGGAGGAGCACTGGA 722
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GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	990	92.5	1424	15	US-10-007-527A-12
4	990	92.5	1424	15	US-10-007-452-12
5	985.2	92.1	1501	9	US-09-791-582-1
6	985.2	92.1	1501	9	US-09-745-476-1
7	985.2	92.1	1501	9	US-09-821-016-5
8	985.2	92.1	1501	9	US-09-748-205-1
9	985.2	92.1	1501	9	US-09-793-920A-1
10	985.2	92.1	1501	10	US-09-951-720-1
11	985.2	92.1	1501	11	US-09-791-610-1
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15	985.2	92.1	1501	15	US-10-266-787-5

16	985.2	92.1	1501	15	US-10-252-518-5	Sequence 5, Appli
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18	985.2	92.1	1501	15	US-10-133-404A-1	Sequence 1, Appli
19	907.4	84.8	1457	9	US-09-726-774-3	Sequence 3, Appli
20	856	80.0	1537	13	US-10-029-397A-46	Sequence 46, Appli
21	832.6	77.8	1481	9	US-09-737-297-4	Sequence 1, Appli
22	830.6	77.6	1486	9	US-09-737-297-1	Sequence 1, Appli
23	820.8	75.4	1506	13	US-10-278-942-1	Sequence 1, Appli
24	807	75.4	1494	14	US-10-007-725-5	Sequence 47, Appli
25	805.4	75.3	1457	13	US-10-029-397A-47	Sequence 35, Appli
26	803.8	75.1	1534	13	US-10-029-397A-35	Sequence 14, Appli
27	801	74.9	1487	9	US-09-726-774-14	Sequence 48, Appli
28	799.6	74.7	1485	13	US-10-029-397A-48	Sequence 158, App
29	798.8	74.7	1506	9	US-09-027-439-3	Sequence 3, Appli
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31	798.4	74.6	1542	11	US-10-061-071-33	Sequence 33, Appli
32	798.4	74.6	1542	15	US-09-027-439-7	Sequence 7, Appli
33	798.2	74.6	1541	9	US-09-027-439-4	Sequence 4, Appli
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39	790.2	73.9	1541	9	US-09-924-868-61	Sequence 81, Appli
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43	783	73.2	1540	15	US-10-260-647-1	Sequence 53, Appli
44	783	73.2	1547	12	US-10-418-861B-53	Sequence 53, Appli
45	782.6	73.1	1547	12	US-10-418-861B-53	Sequence 53, Appli

ALIGNMENTS

Result 1
US-09-737-297-2
Sequence 2, Application US/09737297
Patent No. US20020072108A1
GENERAL INFORMATION:
APPLICANT: Berry, Mark
APPLICANT: Griffiths, Allen
APPLICANT: Hill, Philip
APPLICANT: Laybourne-Parry, Johanna
APPLICANT: Mills, Sarah
TITLE OF INVENTION: Processes and Organisms for the Production of Antifreeze Prote
FILE REFERENCE: F3247
CURRENT FILING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: US/09/737,297
PRIOR FILING DATE: 1999-12-15
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 1070
TYPE: DNA
ORGANISM: Pseudomonas (NCIMB 41076)
US-09-737-297-2

Query Match 100.0%; Score 1070; DB 9; Length 1070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 674 TCCCGGTGTAGCGGTGAATGCGTGAATATAGGAAGGAAACATCTGTGGGAAAGGCA 733
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Db 734 TCTGACACGACTGACAGCTGAGTGGGAAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTA 793
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Qy 896 GAATTAAGGCGGCGCCGACAGCGGTGAGCATGTGTGTTAATTAATTAATTAATTAATTA 955
Db 914 GAATTAAGGCGGCGCCGACAGCGGTGAGCATGTGTGTTAATTAATTAATTAATTAATTA 973
Qy 956 AACCTTAACAGCGCTTGAACATCAATGAATCTTGAAGATTAATTAATTAATTAATTAAT 1015
Db 974 AACCTTAACAGCGCTTGAACATCAATGAATCTTGAAGATTAATTAATTAATTAATTAAT 1033
Qy 1016 CATGAAGACAGGTGCTGATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1068
Db 1034 CCGTGAACAGGTGCTGATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1086

RESULT 14
US-09-602-417-1
Sequence 1, Application US/09602417
Patent No. 6326346
GENERAL INFORMATION:
APPLICANT: Brenchley, Jean E.
APPLICANT: Loveland-Curtze, Jennifer
APPLICANT: Gutshall, Kevin R.
APPLICANT: Humphrey, Vickie L.
TITLE OF INVENTION: Stain Removing Compositions Containing Particular
TITLE OF INVENTION: Isolated and Pure Proteolytic Enzymes
FILE REFERENCE: PS098-2040
CURRENT APPLICATION NUMBER: US/09/602,417
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 1449
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: bacteria

US-09-602-417-1
Query Match 71.4%; Score 764.2; DB 4; Length 1449;
Best Local Similarity 83.8%; Pred. No. 96-260;
Matches 892; Conservative 0; Mismatches 163; Indels 9; Gaps 2;
Qy 15 TGAAGCTGGCGGAGGCTTACATGTAATCGAGGGTGAAGAGAGCTTCTTC 74
Db 1 TGAAGCTGGCGGAGGCTTACATGTAATCGAGGGTGAAGAGAGCTTCTTC 60
Qy 75 TTAAG-----GAGCGGCGAGCGGGTGAAGTATCGTAGAATTCGCTGATGGGG 126
Db 61 CTATAGGTGGGAGAGTGGCGGAGCGGGTGAAGATACATCGGATTAATTTTGTGGGG 120
Qy 127 GATTAAGTTGGAAACGAGCGCTTAATACCGCATACCTCTTAACGGGAGAAAGCGGAGCC 186
Db 121 GATTAAGTTGGAAACCTTAACCGCTTAATACCGCATACCGCTTAACGGGAGAAAGCGGAGCC 180
Qy 187 TTGCGGCGCTTGGCGCTATCAGATGAGCGTATAGTGGATTAAGTGGTGAAGTATGGC 246
Db 181 TTGCGGCGCTTGGCGCTATCAGATGAGCGTATAGTGGATTAAGTGGTGAAGTATGGC 240
Qy 247 TCACCAAGCGAGCATCGCTAACTGATCTGAAGGATGATCACTGGAACCTAGA 306
Db 241 CCACCAAGCGAGCATCGCTAACTGATCTGATGAGGATGATCACTGGAACCTAGA 300
Qy 307 CAGGCTCCAGATCTCTTACCGGAGGAGGAGCATGTGGGAAATTTGACAAATGGCGGAAAGCCT 366
Db 301 CAGGCTCCAGATCTCTTACCGGAGGAGGAGCATGTGGGAAATTTGACAAATGGCGGAGCCT 360
Qy 367 GATCCAGCATGCGCGGTGTGTGAAGAGGTTCTGAGTTGAAGCACTTAATGATGGG 426
Db 361 GATCCAGCATGCGCGGTGTGTGAAGAGGTTCTGAGTTGAAGCACTTAATGATGGG 420
Qy 427 AGAAGGTTGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 486
Db 421 AGAAGGTTGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 480
Qy 487 TTAAGTGTGCGAGCGCGGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 546
Db 481 TTAAGTGTGCGAGCGCGGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 540
Qy 547 GCGTAAAGCGCGGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 606
Db 541 GCGTAAAGCGCGGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 600
Qy 607 GAATTCATTAACAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 666
Db 601 GAATTCATTAACAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Qy 667 GCGTAAAGTGGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 726
Db 661 GCGTAAAGTGGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 720
Qy 727 TACTGACATGAGTGGCGAAAGCGTGGGAGCAACAGATTAATTAATTAATTAATTAATTAAT 786
Db 721 TACTGACATGAGTGGCGAAAGCGTGGGAGCAACAGATTAATTAATTAATTAATTAATTAAT 780
Qy 787 CGCGTAAAGCATGATCACTAGCGGTGAAGC-CTTGAAGCTTTAAGTGGCGAGCTAAC 845
Db 781 CGCGTAAAGCATGATCACTAGCGGTGAAGC-CTTGAAGCTTTAAGTGGCGAGCTAAC 840
Qy 846 GCATTAAAGTTGAAACCGCTTGGGAGTACCGCGGAAAGTTAAATCAATGAATTAAGCGG 905
Db 841 GCATTAAAGTTGAAACCGCTTGGGAGTACCGCGGAAAGTTAAATCAATGAATTAAGCGG 900
Qy 906 GGGCGCGCAAGCGGTGAGCATGTGTTAATTCGAAGCAAGCGGAAAGCTTACCA 965
Db 901 GGGCGCGCAAGCGGTGAGCATGTGTTAATTCGAAGCAAGCGGAAAGCTTACCA 960
Qy 966 GGGCTTGAATCAATGAATCTTGAAGATGATGATGATGATGATGATGATGATGATGATGAT 1025
Db 961 GGGCTTGAATCAATGAATCTTGAAGATGATGATGATGATGATGATGATGATGATGATGAT 1020

APPLICANT: WALKER, Harrell L.
 APPLICANT: HIGGINBOTHAM, Lawrence R.
 TITLE OF INVENTION: CONTROL OF CYANOBACTERIA WITH A BACTERIUM
 FILE REFERENCE: 013243-0007
 CURRENT APPLICATION NUMBER: US/09/228,184
 CURRENT FILING DATE: 1999-01-11
 NUMBER OF SEQ. ID NOS: 1
 SOFTWARE: Patent In Ver. 2.1
 SEQ ID NO: 1
 LENGTH: 1540
 TYPE: DNA
 ORGANISM: Unknown Organism
 FEATURE:
 OTHER INFORMATION: Description of Unknown Organism: Bacterium SG-3;
 OTHER INFORMATION: gram negative, rod-shaped, exhibits flagellate
 OTHER INFORMATION: motility; pathogenic to cyanobacteria and algae;
 OTHER INFORMATION: yellow colonies on BG-11 medium suppl. with tryptic
 US-09-228-184-1

Query Match 73.2%; Score 783; DB 4; Length 1540;
 Best Local Similarity 84.4%; Pred. No. 2,1e-266;
 Matches 906; Conservative 0; Mismatches 160; Indels 7; Gaps 2;

QY	3	CCTTGCTCAGATTGAA	CGCTGGCGGCGAGCCCTAACACATGCAGAGTGGAGCGGTAGAGAGA	62
DB	14	CCTGGCTCAGAGTGAAG	CGCTGGCGGCGAGCCCTAACACATGCAGAGTGGAGCGGACAG	73
QY	63	AGCTTGCTCTCTT	-----GAGAGCGGCGGACGGGTAGTAAATCCCTAGGAATCTGCT	116
DB	74	CAGTAGCAATATCTGTGGTGGGCGAGTGGCGGAGGTAGGAATCATCGGAATCTGCCC	133	
QY	117	GGTAGTGGGGGATTAACGTTTCGGAACGACGCTAATACCGCATAGTCTTACGGAGAAA	176	
DB	134	AGTCGTGGGGGATTAATAGAGGAACTTATGCTAATACCGCATAGGACTTACGGGTGAAA	193	
QY	177	GCAAGGGACCTTGGGCGCTTGGCGCTATCAGATAGCGCTAGAGTGGATTAGTTGGTG	236	
DB	194	GCGGGGGATTCGCAAGACCTTCGCGCATGATGAGCCGATTCGCAATAGCTAGTTGGCG	253	
QY	237	AGGTAAATGGCTCCCAAGGCGAGCATCCGTAATCGTGTGAGAGGATATGATGACACT	296	
DB	254	GCGTAATGGCCCAAGGCGAGCATCCGTAATCGTGTGAGAGGATATGATGACACT	313	
QY	297	GGAATCTGAACACAGCTCCAGACTCTTACCGGAGGACAGAGTGGGGAATATTGACAAATGG	356	
DB	314	GGAATCTGAACACAGCTCCAGACTCTTACCGGAGGACAGAGTGGGGAATATTGACAAATGG	373	
QY	357	GCGAAAGCCTGATCCAGGCGATGCGCGTGTGAGAGAGGTTTCGGATTGTAAGCACT	416	
DB	374	GCGCAAGCCTGATCCAGGCGATGCGCGTGTGAGAGAGGTTTCGGATTGTAAGCACT	433	
QY	417	TTAAGTTGGAGAGAGGTTGATTAATTAATCTGCAATTTTGAAGTTTACCGACAGAT	476	
DB	434	TTTGTCCGAAAGAAAGACATGATTAATTAATCTGCAATTTTGAAGTTTACCGAGAT	493	
QY	477	AAGCAACCGCTAATCTGTGCGACAGACCGCGGTAAATACAGAGGTGTGAACCTTAATCG	536	
DB	494	AAGCAACCGCTAATCTGTGCGACAGACCGCGGTAAATACAGAGGTGTGAACCTTAATCG	553	
QY	537	GAAATTAAGGCGGTAAAGCGCGTAGTGTGTTTGAATTTGATGTAATCCCGGG	596	
DB	554	GAAATTAAGGCGGTAAAGCGGTGATGTTGTTTGAATTTGATGTAATCCCGGG	613	
QY	597	CTCAACCTGGGAACCTGATTAACAATGATGATGATGATGATGATGATGATGATGAT	656	
DB	614	CTCAACCTGGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	673	
QY	657	TTCTGTGTAGCGGTGAATGCGTGAATTAAGAGAGAACCAAGTGGCGAGAGCGCA	716	
DB	674	TCCCGGTGTAGCGGTGAATGCGTGAATGCGTGAATGCGTGAATGCGTGAATGCGCA	733	
QY	717	CTGGAATTAATCTGACATGAGGTGCGAAGCGTGGGAGCAACAGATTAGATACC	776	

DB	734	TCTGACACAGACTGACACTGAGGACGAAACCGTGGGAGCAAAACAGATTAGATACC	793
QY	777	TGGTAGTCCAGCCGCTAAACAGATGCACTGACCGTTGGAAGC-CTTGAGATTAGTG	835
DB	794	TGGTAGTCCAGCCCTTAACAGATGCACTGAGTGTGGTGGCAACTAGGACTAGTAT	853
QY	836	CGGAGCTAACGCTTAATTAATGATGATGATGATGATGATGATGATGATGATGAT	895
DB	854	CGAAGCTAACGCTTAATGATGATGATGATGATGATGATGATGATGATGATGAT	913
QY	896	GAAATGACGGGGGCGGACAGACGCGTGGAGCATGTTTAAATGCAACAGCGGAG	955
DB	914	GAAATGACGGGGGCGGACAGACGCGTGGAGCATGTTTAAATGCAACAGCGGAG	973
QY	956	AACCTTACCGGCTTGCATCATCAATGAATCTTTAGAGATAGATTGGTCTTCGGAA	1015
DB	974	AACCTTACCGGCTTGCATCATCAATGAATCTTTAGAGATAGATTGGTCTTCGGAA	1033
QY	1016	CATTGACAGGTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1068
DB	1034	CGTGAACAGGTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1086

RESULT 13
 US-09-967-376-1
 Sequence 1, Application US/09967376
 Patent No. 6482635
 GENERAL INFORMATION:
 APPLICANT: WALKER, Harrell L.
 APPLICANT: HIGGINBOTHAM, Lawrence R.
 TITLE OF INVENTION: CONTROL OF CYANOBACTERIA WITH A BACTERIUM
 FILE REFERENCE: 013243-0007
 CURRENT APPLICATION NUMBER: US/09/967,376
 CURRENT FILING DATE: 2001-09-28
 NUMBER OF SEQ ID NOS: 1
 SOFTWARE: Patent In Ver. 2.1
 SEQ ID NO: 1
 LENGTH: 1540
 TYPE: DNA
 ORGANISM: Unknown Organism
 FEATURE:
 OTHER INFORMATION: Description of Unknown Organism: Bacterium SG-3; gram negative
 OTHER INFORMATION: rod-shaped; exhibits flagellate motility; pathogenic to
 OTHER INFORMATION: cyanobacteria and algae; yellow colonies on BG-11 medium suppl
 OTHER INFORMATION: with tryptic soy
 US-09-967-376-1

Query Match 73.2%; Score 783; DB 4; Length 1540;
 Best Local Similarity 84.4%; Pred. No. 2,1e-266;
 Matches 906; Conservative 0; Mismatches 160; Indels 7; Gaps 2;

QY	3	CCTTGCTCAGATTGAA	CGCTGGCGGCGAGCCCTAACACATGCAGAGTGGAGCGGTAGAGAGA	62
DB	14	CCTGGCTCAGAGTGAAG	CGCTGGCGGCGAGCCCTAACACATGCAGAGTGGAGCGGACAG	73
QY	63	AGCTTGCTCTCTT	-----GAGAGCGGCGGACGGGTAGTAAATCCCTAGGAATCTGCT	116
DB	74	CAGTAGCAATATCTGTGGTGGGCGAGTGGCGGAGGTAGGAATCATCGGAATCTGCCC	133	
QY	117	GGTAGTGGGGGATTAACGTTTCGGAACGACGCTAATACCGCATAGGCTTACGGGAGAAA	176	
DB	134	AGTCGTGGGGGATTAATAGAGGAACTTATGCTAATACCGCATAGGACTTACGGGTGAAA	193	
QY	177	GCAAGGGACCTTGGGCGCTTGGCGCTATCAGATAGCGCTAGAGTGGATTAGTTGGTG	236	
DB	194	GCGGGGGATTCGCAAGACCTTCGCGCATGATGATGATGATGATGATGATGATGATGAT	253	
QY	237	AGGTAAATGGCTCCCAAGGCGAGCATCCGTAATCGTGTGAGAGGATATGATGACACT	296	
DB	254	GCGTAATGGCCCAAGGCGAGCATCCGTAATCGTGTGAGAGGATATGATGACACT	313	
QY	297	GGAATCTGAACACAGCTCCAGACTCTTACCGGAGGACAGAGTGGGGAATATTGACAAATGG	356	

OY	420	AGTTGGAGAGAGAGGGTTGTGATTAATACTCTGCATTTTGAAGTTACGACAGATAAG	479
Db	435	AGUTGGAGAGAGAGGCGAGUAAAGUUAACUUCUGCUNUUVUUGACGUUACCAAGAAUAG	494
OY	480	CACCGGCTAACTCTGTGCCAGCAGCCGCGGTAACTACG-AGGTCGCAAGCTTAATCGGA	538
Db	495	CACCGGCUAACUCUCUGUCCAGCAGCCGCGGUAAUACUGAAGGUCUGACGUUAUCCGA	554
OY	539	ATTACTGAGGCGTAAAGGCGCGTAGTGGTGTGTTAAGTTAGATGAAATCCCGGGCT	598
Db	555	AUUAUCUGGGTGUAAAGCGCGCGUAGGUGUUUGUAAAGUAGUAGUUAUCCCGGCTU	614
OY	599	CAACCTGGGAACTGCGATTCAAAACTGACTGACTAGATAGTGGTAGAGGGTGGAAATTT	658
Db	615	CAACCTUGGGGACUGCAUCCAAUACUCUGACUGAGGAGCGGUAGAGGUGUGGAUUVU	674
OY	659	CCGTGTAAAGGGGAAATGCGTTGATATAGTAAAGAAACACACAGTGGCGGAAGCGACACC	718
Db	675	CCUUGUAGCGGUGAAUUGCGUAGUUAUAGAAAGAAACACAGGUCGCAAGCGACACC	734
OY	719	TGAGCTAATACTGACACTGAGGTGCGAAAAGCGTGGGAGCAAAACAGATTAGATACCTTG	778
Db	735	UCGACUGAUUACUGACCUGAGGUGCGCAAGC-UGGGAAACVAAACAGAUUVUAGUACCUG	793
OY	779	GTACTCCAGCCCGGTAACGATGTCAACTAGCCGTGGAAAGCCTTGAAGCTTTAAGTGGCCG	838
Db	794	GUAAUCCACGCGCGUCAAAGUAGUAGCUGAGCGGUGGAGUCCUUGAGUACUUAUUGGCGC	853
OY	839	AGCTAACGCAATTAAGTTGACCGCGCTGGGAGTAGCGGCGCAAGGTTAAACTCAATGAA	898
Db	854	AG-UAAAGCGAUAAUGUGACCGCUGGGCGUACCGCGCAAGGUUAAACUCAAAGAU	912
OY	899	TTAGCGGGGGCCCGCCACAAAGCGGTGAGCATGTGTTATTCCAGACACCGCAAGAAC	958
Db	913	U--CAAGGGGCGCGCAACCGGUGAGCAUUGUUAUUCGAAANNAAGCGCAAGAAC	969
OY	959	CTTACGAGGCGCTTGACATCCATGAACTTTCTAGAGATGATTGGTGCCTTCGGGAACAT	1018
Db	970	CUUACCUUGGCUUAGCAUUGUCGGAAUUCUUGACAGACAGUAGCAAGGACUUCGGGAUUG	1029
OY	1019	TGAGACAGGTGCTGCATGCTGTCGTCACTCGTGT	1057
Db	1030	GAAACACAGGUGGCGUAGUGGUCGUCAGAGUACAGUGU	1068
RESULT 10			
US-08-632-470-53			
/ Sequence 53: Application US/08632470			
/ Patent No. 5976791			
/ GENERAL INFORMATION:			
/ APPLICANT: MABILAT, CLAUDE			
/ APPLICANT: RAOUlt, DIDIER			
/ TITLE OF INVENTION: NUCLEOTIDE FRAGMENTS CAPABLE OF			
/ TITLE OF INVENTION: HYBRIDIZING SPECIALLY TO RICKETTSIA RONA OR RNA AND			
/ NUMBER OF SEQUENCES: 53			
/ CORRESPONDENCE ADDRESS:			
/ ADDRESSEE: OLIFF & BERRIDGE			
/ STREET: P.O. BOX 19928			
/ CITY: ALEXANDRIA			
/ STATE: VA			
/ COUNTRY: USA			
/ ZIP: 22320			
/ COMPUTER READABLE FORM:			
/ MEDIUM TYPE: Floppy disk			
/ COMPUTER: IBM PC compatible			
/ OPERATING SYSTEM: PC-DOS/MS-DOS			
/ SOFTWARE: Patentin Release #1.0, Version #1.30			
/ CURRENT APPLICATION DATA:			
/ APPLICATION NUMBER: US/08/632,470			
/ FILING DATE: 08-JUL-1996			
/ CLASSIFICATION: 435			

Query Match	73.7%	Score 788.6	DB 2	Length 1484
Beat Local Similarity	84.5%	Pred. No. 2.1e-268		
Matches 905	Conservative 0	Mismatches 159	Indels 7	Gaps 2
<p>ATTORNEY/AGENT INFORMATION: NAME: BERRIDGE, WILLIAM P REGISTRATION NUMBER: 30,024 REFERENCE/DOCKET NUMBER: WPB 38238 TELECOMMUNICATION INFORMATION: TELEPHONE: (703)-836-6400 TELEFAX: (703)-836-2787 INFORMATION FOR SEQ ID NO: 53: SEQUENCE CHARACTERISTICS: LENGTH: 1484 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)</p>				
US-08-632-470-53				
Query	4	CTTGCTCAAGTTGAAAGCGTGGGAGAGGCTTAACACATGCAAGTCAGCGCTGAGAGACA	63	
Db	19	CTGAGCTCAAGTTGAAAGCGTGAAGGCGATCTTTAACAATGCAAGTCCAGCGAGCGACAG	78	
Qy	64	GCTTGGTCTCTT-----GAGAGGGGGGACGGGTAGTAATGCTTAGAAATCTGCTG	117	
Db	79	GAGNCTTCTCTGGCGGGGAGAGATGGGGGACGGGTAGTAATGCTTAGAAATCTTACTT	138	
Qy	118	GTTAGTGGGGGATTAAGCTTGGAAAGGACGCTAATACCGATACGTTCTACGGGAGAAAG	177	
Db	139	GTTAGTGGGGGATTAAGCTTGGGAAACTCGGGCTAATACCGATATCTCTTTGGAGCAAG	198	
Qy	178	CAGAGGACCTTGGGGCTTTGCGCTATCAGATGAGCCTAGGTCCGATTTAGCTAGTTGTA	237	
Db	199	CGGGGATCTTGGACCTCGTGTATTAAGATGAGCCTACGCTTACTTGTGTTGGTGG	258	
Qy	238	GCTAATGCGTCAACAAAGGACATCCGTAATCTGTTGAGAGATGATCACTCACTG	297	
Db	259	GCTAATGCGCTCAACAAAGGACATCCGTAATCTGTTGAGAGATGATCACTCACTG	318	
Qy	298	GACTGAGACAGGCTCCAGTCTCTTACGGGAGCAGAGTGGGAAATTTGGACATGGG	357	
Db	319	GACTGAGACAGGCTCCAGTCTCTTACGGGAGCAGAGTGGGAAATTTGGACATGGG	378	
Qy	358	CGAAGCTGATCCAGCCATGCGCGTGTGTGAAGAAAGTCTTCCGATTTGAACACTT	417	
Db	379	GGAAGCCCTGATCCAGCCATGCGCGTGTGTGAAGAAAGGCTTCCGATTTGAACACTT	438	
Qy	418	TAACTGGGAGGAAAGGTTGATATTAATCTCGCAATTTTGAACCTTACCGACAGATTA	477	
Db	439	TGGTGGGAAATTAATCTCAAGGTAATCTCTGAGGCTTGAACCTTACCGACAGATTA	498	
Qy	478	AGACCGGTTAATCTTGTGCGAGACGCCGCGTAAATACAGAGGTGCAAGCCTTAATGG	537	
Db	499	AGACCGGTTAATCTTGTGCGAGAGCGCGGTAATACAGAGGTGCAAGCCTTAATGG	558	
Qy	538	AATTAAGTGGGCTTAAGCGCGCTAGCTGTTTGTTAAGTGGATGTGAATCCCGCGGC	597	
Db	559	AATTAAGTGGGCTTAAGCGCGCTAGCTGTTTGTTAAGTGGATGTGAATCCCGCGGC	618	
Qy	598	TCAACTGGGAATGCAATTAACATGACTGATTAAGATGTGTAGAGGGGTGTGGAATT	657	
Db	619	TNNCTGGGAATGCAATTAACATGCTGGGATCTTGAATGTGTAGAGGGGTGTGGAATT	678	
Qy	658	TCCGTGTAGCGGTGAATGCGTGTATTAAGAAAGAAACACAGTGGCGAAGCGACAC	717	
Db	679	TCCGTGTAGCGGTGAATGCGTGTATTAAGAAAGAAACACAGTGGCGAAGCGACAC	738	
Qy	718	CTGAGCTAATCTACACCTAGAGGTGCGAAAGCGTGGGAGCAACAGATTAATCACTCT	777	
Db	739	CTGAGCTAATCTACACCTAGAGCGGAAAGCGTGGGAGCAACAGATTAATCACTCT	798	
Qy	778	GGTAGTCAACCCGTAACGATGTCAACTAGACCGTGTGAAGCGCTTGAAGCTTTAGTGGC	837	

60 AAGAGCTTGTCTCT--CTTGAGAGCGCGGAGCGGTGAGTAATGCTTAGAATCTGCTT 116
 Db AAGAGCTTGTCTCTCTCTGCTGAGAGTGGCGGAGCGGTGAGTAATGCTTAGAATCTGCTT 117
 QY 117 GGTAGTGGGGGATACGTTGCGAAACGAGACGCTATACCGCATACGCTCTACCGGAGAA 116
 Db 138 GATGAGAGGGGATACGTTGCGAAACGAGACGCTATACCGCATACGCTCTACCGGAGAA 117
 QY 177 GAGGAGGACCTTCCGCGCTTGGCTATGATGAGAGCTAGGCTGAGTATGCTAGTGGT 236
 Db 198 GAGGAGGACCTTCCGCGCTTGGCTATGATGAGAGCTAGGCTGAGTATGCTAGTGGT 257
 QY 237 AGGTATGAGCTACCAAGGCGAGATCCGTAACGCTAGTGTGAGAGGATGATCAGTCCACT 236
 Db 258 GGTATACGCTCTACTAGCGAGATCCCTAGTGTGAGAGGATGATCAGTCCACT 317
 QY 297 GGAAGTGAACAGCGGTCCAGACTCTCTACGAGAGGAGAGAGTGGGGAATATTGACATG 356
 Db 318 GGAAGTGAACAGCGGTCCAGACTCTCTACGAGAGGAGAGAGTGGGGAATATTGACATG 377
 QY 357 GCGAAGCTGATCCAGGATGCGCGCTGTGAGAGAGGCTTCCGATTTGTAAGACT 416
 Db 378 GCGAAGCTGATCCAGGATGCGCGCTGTGAGAGAGGCTTCCGATTTGTAAGACT 437
 QY 417 TTAGTTGAGAGAGGCTTGTAGATTATCTCTGCAATTTTGAAGCTTACCGACAGAAAT 476
 Db 438 TTAGTTGAGAGAGGCTTGTAGATTATCTCTGCAATTTTGAAGCTTACCGACAGAAAT 497
 QY 477 AAGCAGCGCTTACTCTGTGCGAGAGCGCGGTGTAATACAGAGGCTTCAAGCTTAATG 536
 Db 498 AAGCAGCGCTTACTCTGTGCGAGAGCGCGGTGTAATACAGAGGCTTCAAGCTTAATG 557
 QY 537 GAATTAAGTGGGCTTAAAGCGCGCTAGGCTTGTGTAAGTGGATGTAATCCCGGAG 596
 Db 558 GAATTAAGTGGGCTTAAAGCGCGCTAGGCTTGTGTAAGTGGATGTAATCCCGGAG 617
 QY 597 CTCAAGCTTGGAACTGCAATTCAAACTGACTAGTATGATGAGAGGCTTGGTGAAT 656
 Db 618 CTCAAGCTTGGAACTGCAATTCAAACTGACTAGTATGATGAGAGGCTTGGTGAAT 677
 QY 657 TTCTGTGAGAGGCTTAAAGCGCGCTAGGCTTGTGTAAGTGGATGTAATCCCGGAG 716
 Db 678 TTCTGTGAGAGGCTTAAAGCGCGCTAGGCTTGTGTAAGTGGATGTAATCCCGGAG 737
 QY 717 CCTGAGTAAATGCTGACACTGAGGCTGCGAAACGCTGGGAGCAAAACGATTAATCC 776
 Db 738 CCTGAGTAAATGCTGACACTGAGGCTGCGAAACGCTGGGAGCAAAACGATTAATCC 797
 QY 777 TGTGATCCAGCGCGCTTAAAGCGCGCTAGGCTTGAAGCTTGAAGCTTTTGAAGTGC 836
 Db 798 TGTGATCCAGCGCGCTTAAAGCGCGCTAGGCTTGAAGCTTGAAGCTTTTGAAGTGC 857
 QY 837 GCAGCTAAAGCTTAAAGTGAACGCTGCGGAGTACGCGCGCAAGGTTAAATCTCAATG 896
 Db 858 GCAGCTAAAGCTTAAAGTGAACGCTGCGGAGTACGCGCGCAAGGTTAAATCTCAATG 917
 QY 897 AATTGACGCGCGCGCTTAAAGCGCGCTAGGCTTGAAGCTTGAAGCTTTTGAAGTGC 956
 Db 918 AATTGACGCGCGCGCTTAAAGCGCGCTAGGCTTGAAGCTTGAAGCTTTTGAAGTGC 977
 QY 957 AACTTACGAGCGCTTGAACATCCATGAACTTTCTAGAGATGATGTTGGTCTTCCGGAAC 1016
 Db 978 AACTTACGAGCGCTTGAACATCCATGAACTTTCTAGAGATGATGTTGGTCTTCCGGAAC 1037
 QY 1017 AATTGACGAGTGTGCTGATGCTGTCTGCTGCTGTGTGTAATGTAAG 1068
 Db 1038 CGTAGACAGGCTGTGCTGATGCTGTCTGCTGCTGTGTGTAATGTAAG 1089

RESULT 9
 US-08-114-695A-2
 Sequence 2, Application US/08114695A

Patent No. 5508193
 GENERAL INFORMATION:
 APPLICANT: Mandelbaum, Raphael T.
 APPLICANT: Wacker, Lawrence P.
 TITLE OF INVENTION: DEGRADATION OF S-TRIAZINES IN SOIL AND
 TITLE OF INVENTION: WATER
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SCHWEGMAN, LUNDBERG & WOESSNER, P.A.
 STREET: 3500 IDS CENTER
 CITY: MINNEAPOLIS
 STATE: MN
 COUNTRY: USA
 ZIP: 55402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/114,695A
 FILING DATE: 31-AUG-1993
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: MUELLING, ANN M.
 REGISTRATION NUMBER: 33,977
 REFERENCE/DOCKET NUMBER: 600,268US1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 612-339-0331
 TELEFAX: 612-339-3061
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1473 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: rRNA
 ORIGINAL SOURCE:
 ORGANISM: Pseudomonas sp. Atrazine-Degrading Isolate
 ORGANISM:
 US-08-114-695A-2

Query Match 74.1%; Score 793.4; DB 1; Length 1473;
 Best Local Similarity 70.0%; Pred. No. 4,3e-270;
 Matches 741; Conservative 198; Mismatches 111; Indels 9; Gaps 7;

3 CCTGTGCTCAGATGAAAGCTGAGCGG--CAGGCTTAAACATGCAAGTCAAGCGGTAGAGAG 61
 15 CAUGGCTCAUAUAGUAUUGGCGGUAAGCCUAACAUGCAAGUCGAGCGGAGUAAG 74
 Db 62 AAGCTTCTCTCTTGAG-AGCGGCGAGCGGTGAGTAATGCTTGAAGATCTGCTG-T 119
 QY 75 GAGCUCUCUCGCGGAAUUAUGCGCGGAGUGGUAUUAUGCUCUAGGAAUUCUGCUGGU 134
 Db 120 AGTGGGGGATTAAGTTGGGAAACGAGCGTAAATACCGCATAGCTCTAGGAGAAAGCA 179
 QY 135 AGUGGGGAGCAAGCUCUCCGAAAGAGCGCUAUAACCGCAUAGUCUCCGAGGAAAGUG 194
 Db 180 GGGGACCTTGGGCGCTTGCCTATCAGATGAGCTAGTCCGATTAAGTATGATGTTGAG 239
 QY 195 GGGGAAUUCUGGAGCUCUCCGAAAGAGCGCUAUAAGCGGAGGCGGAAUUAUGUAGUGGG 254
 Db 240 TAAATGCTCAAGAGGAGAGAGTCCGTAATGCTGAGAGATGATGATGATGATGATGATG 299
 QY 255 UAAUGGCUACUAAGGAGAGAGCUGAAUCUGGUCUAGAGAGUAGUAGUAGUAGUAGUAG 314
 Db 300 ACTGAGACAGGCTCAGACTCTTACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 359
 QY 315 ACUGAGACAGGCTCAGACTCTTACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 374
 Db 360 AAGGCTGATCCAGGATGCGCGGTGTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 419
 QY 375 AAGGCTGATCCAGGATGCGCGGTGTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 434

Query Match	74.6%;	Score 798.4;	DB 4;	Length 1542;
Best Local Similarity	68.2%;	Pred. No. 7.5e-272;		
Matches 731;	Conservative 184;	Mismatches 151;	Inbels 6;	Gaps 2

Db	738	CCUGACGAAGACUGACGCTCAGUGGCGAAGAGCGUGGGAGCAAAACAGAUUAGUACC	799
Qy	777	TGGTATCCAGCCCTTAACAGATGTCACTACCCCTTTGAAGCCTTGACCTTTTGTGC	836
Db	798	UGGUAUCCAGCCCGUAAACAGAUUGCAUUGAGGUGGCCUUGAGCGGUCUCC	857
Qy	837	GCAGCTAACGCATTAAAGTTGACCGCCTGGGAGTAACGCGCAAGGTTAACTCAATG	896
Db	858	GAGGCUAAGCGCUVAAAGUCAGCCGCTUGGGAGUACGCGCGCAAGGUUAAACUCAAU	917
Qy	897	AATTACCGGGGGCCCGCAGCGGCTGACATGCTGTTTAAATCGAACCAACGGGAAG	956
Db	918	AATUAGCGGGGCGCCGCAAGCGGAGACAGUGGUTUUAUUCAUCAACGCAAGCA	977
Qy	957	ACCTTACGAGCCTTGACATGCAATGACTTTCTAGATAGATAGTTGGTCCCTCGGAAC	1016
Db	978	ACCUAACCTGAGCTUUGACATCCACGGAAGUUAUUCAGAAAGUAGUCCUUCGGGAC	1037
Qy	1017	ATTGAGACGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1068
Db	1038	CGUGACAGCGGCTGCGACUGGCTGCGACGCTGCGACGCTGCGACGCTGCGACGCTGCG	1089
Db	1038	CGUGACAGCGGCTGCGACUGGCTGCGACGCTGCGACGCTGCGACGCTGCGACGCTGCG	1089
RESULT 8			
	US-08-520-946-158		
	Sequence 158, Application US/08520946		
	Patent No. 6372424		
	GENERAL INFORMATION:		
	APPLICANT: BROW, MARY ANN D.		
	APPLICANT: LYAMICHEV, VICTOR I.		
	APPLICANT: OLIVE, DAVID M.		
	TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF		
	TITLE OF INVENTION: PATHOGENS		
	NUMBER OF SEQUENCES: 160		
	CORRESPONDENCE ADDRESS:		
	ADDRESSER: MEDLEN & CARROLL		
	STREET: 220 MONTGOMERY STREET, SUITE 2200		
	CITY: SAN FRANCISCO		
	STATE: CALIFORNIA		
	COUNTRY: UNITED STATES OF AMERICA		
	ZIP: 94104		
	COMPUTER READABLE FORM:		
	MEDIUM TYPE: Floppy disk		
	COMPUTER: IBM PC Compatible		
	OPERATING SYSTEM: PC-DOS/MS-DOS		
	SOFTWARE: PatentIn Release #1.0, Version #1.25		
	CURRENT APPLICATION DATA:		
	APPLICATION NUMBER: US/08/520.946		
	FILING DATE:		
	CLASSIFICATION: 435		
	ATTORNEY/AGENT INFORMATION:		
	NAME: CARROLL, PETER G		
	REGISTRATION NUMBER: 32,837		
	REFERENCE/DOCKET NUMBER: FORS-01756		
	TELECOMMUNICATION INFORMATION:		
	TELEPHONE: (415) 705-8410		
	TELEFAX: (415) 337-8338		
	INFORMATION FOR SEQ ID NO: 158:		
	SEQUENCE CHARACTERISTICS:		
	LENGTH: 1542 base pairs		
	TYPE: nucleic acid		
	STRANDEDNESS: double		
	TOPOLOGY: linear		
	MOLECULE TYPE: DNA (genomic)		
	US-08-520-946-158		
	Query Match	74.6%;	Score 798.4; DB 4; Length 1542;
	Best Local Similarity	85.4%;	Pred. No. 7.5e-272;
	Matches 915; Conservative 0; Mismatches 151; Indels 6; Gaps 2;		
Qy	3	CCTGCTCATATTGACGCTTGGCGGCGAGGCTTAACACATGACGAAGTGACGGGT--AGAG	59
Db	18	CATGCTCAGATTAGACGCTTGGCGGCGAGGCTTAACACATGACGAAGTGACGAAGTAA	77


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Db      481  TGCCAGCAGCCGCGTAAATACAGAGGGTGCAAAGCGTTAAATGGAATTAACTGGGGCTTAAAG 540
OY      555  CGCGCGTAAAGTGGTTTGTATTAGTTGATATGTGAAATCCCCGGGCTCAACTGGGAATCTCA 614
Db      541  CGCCCGTAAAGTGGTTTGTATTAGTTGATATGTGAAATCCCCGGGCTCAACTGGGAATCTCA 600
OY      615  TTCAAAACTGACTGACTAGATATGAGTAAAGGGTGTGGAATTTCTGTATAGCGGTGAA 674
Db      601  TTCAAACTGACAAGCTAGAGTATGAGTAAAGGGTGTGGAATTTCTGTATAGCGGTGAA 660
OY      675  ATGGGTGATATATGGAAGGAACAACAAGTGGCGAAGCGCAACAAGCTGATCTTAATCTGACA 734
Db      661  ATGGGTGATATATGGAAGGAACAACAAGTGGCGAAGCGCAACAAGCTGATCTTAATCTGACA 720
OY      735  CTGAGGTGCGAAAAGCGTGGGGAGCAAAACAGATTGATACCTGTAGTCCAGCGCGTAA 794
Db      721  CTGAGGTGCGAAAAGCGTGGGGAGCAAAACAGATTGATACCTGTAGTCCAGCGCGTAA 780
OY      795  ACGATGTCAACTGACCGGTTGGAAGCCTTGAGCTTTAATGGCGAGCTAAGCATTAAGT 854
Db      781  ACGATGTCAACTGACCGGTTGGAAGCCTTGAGCTTTAATGGCGAGCTAAGCATTAAGT 840
OY      855  TGACCGCGTGGGGAGTACGCGCCGCAAGGTTAAACTCAATGAATTGACGGGGCCCGCA 914
Db      841  TGACCGCGTGGGGAGTACGCGCCGCAAGGTTAAACTCAATGAATTGACGGGGCCCGCA 900
OY      915  CAAGCGGTGAGGAGATGGTTTAATTCGAGCAACGGGAAGAACTTACAGAGGCTTGAC 974
Db      901  CAAGCGGTGAGGAGATGGTTTAATTCGAGCAACGGGAAGAACTTACAGAGGCTTGAC 960
OY      975  ATCCATGAACCTTTCTAGAGATAGATTGGTGCTTCGGGAACATTGAGACAGGTGCTGCA 1033
Db      961  ATCCATGAACCTTTCCAGAGATAGATTGGTGCTTCGGGAACATTGAGACAGGTGCTGCA 1022
OY      1035  TGGCTGTGCTCAGCTCGTGTGTAATGTAAG 1068
Db      1021  TGGCTGTGCTCAGCTCGTGTGTAATGTAAG 1054

RESULT 5
US-08-114-695A-6
: Sequence 6, Application US/08114695A
: Patent No. 5508193
: GENERAL INFORMATION:
: APPLICANT: Mandelbaum, Raphael T.
: APPLICANT: Mackette, Lawrence P.
: TITLE OF INVENTION: DEGRADATION OF S-TRIAZINES IN SOIL AND
: TITLE OF INVENTION: WATER
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SCHWEGMAN, LUNDBERG & WOESSNER, P.A.
: STREET: 3500 IDS CENTER
: CITY: MINNEAPOLIS
: STATE: MN
: COUNTRY: USA
: ZIP: 55402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA
: APPLICATION NUMBER: US/08/114,695A
: FILING DATE: 31-AUG-1993
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: MUELLING, ANN M.
: REGISTRATION NUMBER: 33,977
: REFERENCE/DOCKET NUMBER: 600,268US1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 612-333-0331
: TELEFAX: 612-339-3061
: INFORMATION FOR SEQ ID NO: 6:

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Query Match	86.0%	Score 920.4	DB 1	Length 1518
Best Local Similarity	73.0%	Fred. No. 6.2e-315		
Matches 779	Conservative 201	Mismatches 86	Indels 1	Gaps 1
SEQUENCE CHARACTERISTICS: LENGTH: 1518 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: rRNA ORIGINAL SOURCE: ORGANISM: <i>Pseudomonas aeruginosa</i> US-08-114-695A-6				
QY	3	CCTTGTGCAGATTGTAACGCTGCGGACAG-GCCTAACACATGACAAAGTCGACGCGTAGAGAG	61	
Db	18	CAUGGCUCAAGUUAAGCGUGCCGACAGNCGCUAACACAUICAAAGUCGACGCGAGUAGAG	77	
QY	62	AAGCTTGCCTTCTTCTTGAAGAAGCGCGGACGCGGTAGTAAATGCTTGAAGATCTGCGTGTG	121	
Db	78	GACGCUUGCUCUGAUAUUCAGCGCGGACGCGGUGUAUUCCTAAGGAACUUCGCGAAG	137	
QY	122	TGGGAGATTAACCTTTCGAAACGACGCGCTAAATACCGCATAGTCTCTACGCGAGAAACAG	181	
Db	138	UGGGAGUAUACGUCGCGAAACGGGCGCUAAUCCGCAUAGUCUUAAGGAGAAAGGGG	197	
QY	182	GGACCTTGGGGGCTTGGCCCTATCAAGTAGCCTTAGTGGATTAGTACTAGTGTGAGTA	241	
Db	198	GGUCCUGGAGACCUACACGCUAUCGAGAGACCUAGGCGGAUAGCUAUGUUGUGGGUA	257	
QY	242	ATGGCTCAACAAAGGCGAGATCCGTAACGTGCTGAGAGGATGATCATGACATGCAAC	301	
Db	258	AAGGCUAACAAAGGCGAGCGAUCGCUAAUCUGGUCUGAAGGACGUAUCAGUACACUCGAGAC	317	
QY	302	TGAGAACGCTTCACACCTCTTACGGGAGGACGACGTGGGAAATATTGACATATGGCGGA	361	
Db	318	UGAGACACGGUCACACUCCUACGCGAGGACGACGUGGGAAUAVUGAACAUUGGCGAA	377	
QY	362	AGCCTGATCAACCCATGCGCGGTGTGAAAGAGCTTCGCGATTGTAAAGCATTTAAG	421	
Db	378	AGCGAUAUCACGACCAUGCCGCGUGUGUAGAAAGGUCUUCGAGUUSUAAAGCAUUAAG	437	
QY	422	TGGGAGGAAGGCTGTGAATTAATCTCTGCAATTTTGACGTTTACCCAGACAAATAGCA	481	
Db	438	UUGGAGGAGAGGACGUAUUAUACUUCUGUGUUAUGCUAACCAACAAUAAACCA	497	
QY	482	CCGCGTAATCTGTGTCACGACGCGCGGTAAATCAAGAGGTGCAAGCCTTAATCGAATT	541	
Db	498	CCGGCUAACUUCUGGCCGACGCGCGGUAUUAAGAAAGGUGGACGUAUUCGGAU	557	
QY	542	ACTGGGCGTAAAGCGCGGTAGGTGCTTTGTTAAGTTGATGTGAATATCCCGGGCTCA	601	
Db	558	ACUGGCGUAAAGCGCGGUAUUAUAGGUAUACGAAUGUGUAGAAUUCGCCGGCUAA	617	
QY	602	CCTGGGAACTGCAATTAACAACTGACTACTAGAGTAGTGTGTAAGGGTGTGCAATTTCT	661	
Db	618	CCUGGGAACUGAUCUAAACUAACUAGCUAGAGUAGGUAAGGUGUGGAUUTUCU	677	
QY	662	GCTGAGCGGTAAATGCGTAGATTAAGAAAGGAACCACTGGCCGAAGCGCACCTGCG	721	
Db	678	GUGUAGCGGUAAUUGCUAAUUAAGAAAGAACCAAGUGGCGAAAGCGCACCTGCG	737	
QY	722	ACTAACTATGACACTGAGGTGCGAAACGTGCGGACCAACAGAGATTAGATACCTGCTA	781	
Db	738	ACUGAACUGACACUGAGUGCGAAACGUGGGAGCAAAACAGAUUAGAUUCCUGUA	797	
QY	782	GTCCAGCGCGTAAACGATGTCACATGACCGTGGGAGCCTTGAAGCTTTAGTGGCGAGC	841	
Db	798	GUCCACGCGCGTAAACGAGUGUAGUACCGUUGGAGUCCUUAAGAUUAGUGGCGCAGC	857	
QY	842	TAAACCATTAAGTTAGCCGCTGCGAGTAGCGCGCAAGGTTAAATCAATGAATTG	901	
Db	858	UAAACCGAUAUUGACGCGCUGGAGGUAUCCGCGCCGAAAGUUAUAACTCAAAUAGUATG	917	

APPLICANT: CANON INC.
TITLE OF INVENTION: Preparation of Poly-hydroxyalkanoic Acid
FILE REFERENCE: 4351008
CURRENT APPLICATION NUMBER: US/09/745,476
CURRENT FILING DATE: 2000-12-26
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Microsoft Word
SEQ ID NO: 1
LENGTH: 1501
TYPE: DNA
ORGANISM: Pseudomonas jessenii 161 ; FERM P-17445
US-09-745-476-1

Query Match 92.1% Score 985.2; DB 4; Length 1501;
Best Local Similarity 95.9%; Pred. No. 0;
Matches 1011; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

15 TGAACGCTGGCGGCGGCTTAACACATGCAAGTCGAGCGGTAGAGAAAGCTTGTCTC 74
1 TGAACGCTGGCGGCGGCTTAACACATGCAAGTCGAGCGGTAGAGAAAGCTTGTCTC 60
75 TTGAGAGCGGCGGCGGCTTAACATGCTAGAAATGCTGCTGTTGGGGATTAAGT 134
61 AATTGACGCGGCGGCGGCTTAACATGCTAGAAATGCTGCTGTTGGGGATTAAGT 120
135 TCGGAAACGCGGCTTAACATGCTAGAAATGCTGCTGTTGGGGATTAAGT 194
121 CTGGAAGGGAAGCTTAACATGCTAGAAATGCTGCTGTTGGGGATTAAGT 180
195 TTGGCTATCAGATGAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 254
181 TTGGCTATCAGATGAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
255 GCGAGATCCGCTTAACATGCTGAGAGATGCTGCTGCTGCTGCTGCTGCTGCT 314
241 GCGAGATCCGCTTAACATGCTGAGAGATGCTGCTGCTGCTGCTGCTGCTGCT 300
315 AGACTCTTAACGAGGCGGCTTAACATGCTGAGAGATGCTGCTGCTGCTGCTGCT 374
301 AGACTCTTAACGAGGCGGCTTAACATGCTGAGAGATGCTGCTGCTGCTGCTGCT 360
375 CATGCCGCTGCTGAGAGAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 434
361 CATGCCGCTGCTGAGAGAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
435 TTGAGATTAACTCTGCAATTTTGAAGTTTGAAGTTTGAAGTTTGAAGTTTGAAG 494
421 CATTAACCTAATAGTTAGTTTGAAGTTTGAAGTTTGAAGTTTGAAGTTTGAAG 480
495 TCGGAAACGCGGCTTAACATGCTGAGAGATGCTGCTGCTGCTGCTGCTGCTGCT 554
481 TCGGAAACGCGGCTTAACATGCTGAGAGATGCTGCTGCTGCTGCTGCTGCTGCT 540
555 GCGAGATCCGCTTAACATGCTGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 614
541 GCGAGATCCGCTTAACATGCTGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
615 TTGAAACTGACTGATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGT 674
601 TTGAAACTGACTGATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGT 660
675 ATGCGTATGATATGAGGAGAAACATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 734
661 ATGCGTATGATATGAGGAGAAACATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
735 CTGAGTTCGCGGAG 794
721 CTGAGTTCGCGGAG 780
795 ACGATGCTAATGAG 854
781 ACGATGCTAATGAG 840

855 TGAACGCTGGCGGCGGCTTAACACATGCAAGTCGAGCGGTAGAGAAAGCTTGTCTC 914
841 TGAACGCTGGCGGCGGCTTAACACATGCAAGTCGAGCGGTAGAGAAAGCTTGTCTC 900
915 CAAGCGGTGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 974
901 CAAGCGGTGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
975 ATCCATGAACTTTCTAGAGATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1034
961 ATCCATGAACTTTCTAGAGATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
1035 TGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1068
1021 TGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1054

RESULT 4

US-09-748-205-1
Sequence 1, Application US/09748205
Patent No. 6586562

GENERAL INFORMATION:
APPLICANT: Canon Inc.
TITLE OF INVENTION: Polyhydroxyalkanoate its manufacturing method, and microorganism
FILE REFERENCE: 4351009
CURRENT APPLICATION NUMBER: US/09/748,205
CURRENT FILING DATE: 2000-12-27
NUMBER OF SEQ ID NOS: 1
SEQ ID NO: 1
LENGTH: 1501
TYPE: DNA
ORGANISM: Pseudomonas jessenii 161 strain.
US-09-748-205-1

Query Match 92.1% Score 985.2; DB 4; Length 1501;
Best Local Similarity 95.9%; Pred. No. 0;
Matches 1011; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

15 TGAACGCTGGCGGCGGCTTAACACATGCAAGTCGAGCGGTAGAGAAAGCTTGTCTC 74
1 TGAACGCTGGCGGCGGCTTAACACATGCAAGTCGAGCGGTAGAGAAAGCTTGTCTC 60
75 TTGAGAGCGGCGGCGGCTTAACATGCTAGAAATGCTGCTGTTGGGGATTAAGT 134
61 AATTGACGCGGCGGCGGCTTAACATGCTAGAAATGCTGCTGTTGGGGATTAAGT 120
135 TCGGAAACGCGGCTTAACATGCTAGAAATGCTGCTGTTGGGGATTAAGT 194
121 CTGGAAGGGAAGCTTAACATGCTAGAAATGCTGCTGTTGGGGATTAAGT 180
195 TTGGCTATCAGATGAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 254
181 TTGGCTATCAGATGAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
255 GCGAGATCCGCTTAACATGCTGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 314
241 GCGAGATCCGCTTAACATGCTGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
315 AGACTCTTAACGAGGCGGCTTAACATGCTGAGAGATGCTGCTGCTGCTGCTGCTGCT 374
301 AGACTCTTAACGAGGCGGCTTAACATGCTGAGAGATGCTGCTGCTGCTGCTGCTGCT 360
375 CATGCCGCTGCTGAGAGAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 434
361 CATGCCGCTGCTGAGAGAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
435 TTGAGATTAACTCTGCAATTTTGAAGTTTGAAGTTTGAAGTTTGAAGTTTGAAG 494
421 CATTAACCTAATAGTTAGTTTGAAGTTTGAAGTTTGAAGTTTGAAGTTTGAAG 480
495 TCGGAAACGCGGCTTAACATGCTGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 554

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OY 435 TTGAGATTAACTCTGCACATTTTGACGTACCGACAGAAATAGAACCGCGCTAACTCG 494
Db 421 CATTAACCTAATAGGTAGTGTGTTTGACGTTTACCGACAGAAATAGAACCGCGCTAACTCG 480
OY 495 TGCACAGACCGCGCGTAAATACAGAGGGTGCAGAGCGTTAATCGAATTAATCTGGCGCTAAAG 554
Db 481 TGCCACAGCGCGCGGTAAATACAGAGGGTGCAGAGCGTTAATCGAATTAATCTGGCGCTAAAG 540
OY 555 CGCGCGTATGGTGTGTTGTTAAGTTGGATATGGAAATCCCGGGGTCAACCTGGGAAATCGCA 614
Db 541 CGCGCGTATGGTGTGTTGTTAAGTTGGATATGGAAATCCCGGGGTCAACCTGGGAAATCGCA 600
OY 615 TTCAAAATCTGACTAGAGTATGTATAGAGGGTGTGTGTAATTTCCGTGTATGCGGTGAA 674
Db 601 TTCAAAATCTGACAAGCTAGAGTATGTATAGAGGGTGTGTGTAATTTCCGTGTATGCGGTGAA 660
OY 675 ATGCGGTATATTTAGGAAGAGAAACACCACTGGCGAAAGCGACACCACTGACTAATATCTGACA 734
Db 661 ATGCGGTATATTTAGGAAGAGAAACACCACTGGCGAAAGCGACACCACTGACTAATATCTGACA 720
OY 735 CTGAGGTGCGAAACCGTGGGGGCAAAACAGAAATTAGTACCTGTGTAGTCCAGCGCGTAA 794
Db 721 CTGAGGTGCGAAACCGTGGGGGCAAAACAGAAATTAGTATACCTGTGTAGTCCAGCGCGTAA 780
OY 795 ACGATGTCAATTAACCGCTTGGAGACCTTTGAGCTTTTATGTGTGGCGACCTAACCGATTAACT 854
Db 781 ACGATGTCAATTAACCGCTTGGAGACCTTTGAGCTTTTATGTGTGGCGACCTAACCGATTAACT 840
OY 855 TGACCGCGCTGGGGGAGTACGGCGCGCAAGTTAAACTCAATGTAATGACGGGGGGCCCGCA 914
Db 841 TGACCGCGCTGGGGGAGTACGGCGCGCAAGTTAAACTCAATGTAATGACGGGGGGCCCGCA 900
OY 915 CAACCGGTGAGACATGTGTGTTTAATTGAAAGCAACGGAGAAACCTTAACAGAGCTTGAC 974
Db 901 CAACCGGTGAGACATGTGTGTTTAATTGAAAGCAACGGAGAAACCTTAACAGAGCTTGAC 960
OY 975 ATCCAAATGAATTTCTAGAAATAGATGTGTGCTTTGGGAACTTTAGACAGAGTGTGCA 1034
Db 961 ATCCAAATGAATTTCTAGAAATAGATGTGTGCTTTGGGAACTTTAGACAGAGTGTGCA 1020
OY 1035 TGCGTGTGCTAGCTCGTGTGTTGAAATGTAAAG 1068
Db 1021 TGCGTGTGCTAGCTCGTGTGTTGAAATGTAAAG 1054

RESULT 2
US-09-821-016-5
; Sequence 5, Application US/09821016
; Patent No. 6485951
; GENERAL INFORMATION:
; APPLICANT: CANON INC.
; TITLE OF INVENTION: Polyhydroxyalkanoate Synthase and Gene Encoding the Same Enzyme
; FILE REFERENCE: 4051021
; CURRENT APPLICATION NUMBER: US/09/821,016
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Microsoft Word
; SEQ ID NO 5
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii Pl61 ; BP-7376
; FEATURE:
; US-09-821-016-5

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Db	61	AATTCAAGCGCGGACGGGTGAATTAAGCTTAGAGAAATGCTCGTGTGTGGGGACAACT	120
QY	135	TCGGAAACGGAAGCTAATACCGCATACGCTCTTACGGGAGAAAGCAGGGACCTTCGGGCG	194
Db	121	CTCGAAAGGGAAGCTAATACCGCATACGCTCTTACGGGAGAAAGCAGGGACCTTCGGGCG	180
QY	195	TTGCGGTATCAATAGAGCTTAGTTCGATTAAGCTAAGTGGTAGGTAATAGGCTCACCAAG	254
Db	181	TTGCGGTATCAATAGAGCTTAGTTCGATTAAGCTAAGTGGTAGGTAATAGGCTCACCAAG	240
QY	255	GCACGATCCGTAACTGCTCTGAGAGATGATCAGTCACTCGAACTGAGACAGGTC	314
Db	241	GCACGATCCGTAACTGCTCTGAGAGATGATCAGTCACTCGAACTGAGACAGGTC	300
QY	315	AGAATCTTACGGGAGGACAGTGGGAAATTTGGACAAATGGCGAAACCTGATCCAGC	374
Db	301	AGAATCTTACGGGAGGACAGTGGGAAATTTGGACAAATGGCGAAACCTGATCCAGC	360
QY	375	CATGCCGCGTGTGTAAGAGGTCCTGCGAATTTGAAAGCACTTAAGTTGGAGGAAGG	434
Db	361	CATGCCGCGTGTGTAAGAGGTCCTGCGAATTTGAAAGCACTTAAGTTGGAGGAAGG	420
QY	435	TTGTAGATTAACTCTGCAATTTTGAAGTTACCGACAGATNAGCACCGCATTACTG	494
Db	421	CATTAACTTAATAGCTTAGTGTGTTGAAGTTACCGACAGATNAGCACCGCATTACTG	480
QY	495	TGCGACACCGCGGTAAATACAGAGGTGCACAGCTTAATCGGAATTAATGAGGCTAAG	554
Db	481	TGCGACACCGCGGTAAATACAGAGGTGCACAGGTTAAATCGGAATTAATGAGGCTAAG	540
QY	555	CGCGCTAGTGTGTTGTAAGTTGAAATGTAATCCCGGCGCTCAACTGCGGAATCTCA	614
Db	541	CGCGCTAGTGTGTTGTAAGTTGAAATGTAATCCCGGCGCTCAACTGCGGAATCTCA	600
QY	615	TTCAAAACTGACTGACTGAATATGTAAGAGGTGTGGAATTTCTGTGTAGCGGTAA	674
Db	601	TTCAAAACTGACTGACTGAATATGTAAGAGGTGTGGAATTTCTGTGTAGCGGTAA	660
QY	675	ATCGTAGATTAGGAAGAACACAGTGGCGAAAGCGAACCTGGAATAATCTAGCA	734
Db	661	ATCGTAGATTAGGAAGAACACAGTGGCGAAAGCGAACCTGGAATAATCTAGCA	720
QY	735	CTGAGGTGCGAATAGCTGTGGGAGCAACAGAGTTAATACCTGTGATGCAAGCGGTAA	794
Db	721	CTGAGGTGCGAATAGCTGTGGGAGCAACAGAGTTAATACCTGTGATGCAAGCGGTAA	780
QY	795	ACGATGTCAACTAGCCGTGGAAGCCCTTAAAGCTTTAAGTGGCGGACCTAACGATTAAGT	854
Db	781	ACGATGTCAACTAGCCGTGGAAGCCCTTAAAGCTTTAAGTGGCGGACCTAACGATTAAGT	840
QY	855	TGACCGCTGTGGGAGTAAGCGCCGACAGGTTAAACTCAATGATATGACGGGGGCGCGCA	914
Db	841	TGACCGCTGTGGGAGTAAGCGCCGACAGGTTAAACTCAATGATATGACGGGGGCGCGCA	900
QY	915	CAAGCGGTGAGACATGTGTTAATTGAAAGCAACCGGAATCTTACAGGCTTGAAC	974
Db	901	CAAGCGGTGAGACATGTGTTAATTGAAAGCAACCGGAATCTTACAGGCTTGAAC	960
QY	975	ATCCATGAACTTTCTAGATATGATGTGTCCTTGGGGAACATTGAGACAGTGTCTCA	1034
Db	961	ATCCATGAACTTTCTAGATATGATGTGTCCTTGGGGAACATTGAGACAGTGTCTCA	1020
QY	1035	TGCTGTGTGTAAGCTCGTGTGTGTAATGTAAAG	1068
Db	1021	TGCTGTGTGTAAGCTCGTGTGTGTAATGTGAG	1054


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OY 639 GGTAGAGGGTGTGGAATTTCTGTGTAGCGGTGAATGTAGATATAGAGAGACAC 698
    |||
Db 413 GGTAGGGGGCAGAGGGAATTTCCGGTGGAGCGGTGAATGTGTAGATCGGAAGAACAC 354
    |||
OY 699 CAGTGGGGAAAGGCGACACCTGAGCTAATCTGACACTGAGGTGGGAAGCGTGGGGAGC 758
    |||
Db 353 CAACGGCGAAGACCTTGTCTGGGCGACCTGACACTGAGACCTGAGACCGAAGCTTAGGGGAGC 294
    |||
OY 759 AAACAGGATTAGATACCTGTGTAGTCCACGCCGTAAACGATGTCACTAGCCGTGGAAG 818
    |||
Db 293 GAATGGATTAGATACCCGAGTAGTCTTAGCCGTAAACGATGTACTAGCGCTGTGG 234
    |||
OY 819 CCTTGA-GCTTTAGTGGCCGACGTAAACGATTAAGTTGACCGCCTGGGGAGTAGCGCG 877
    |||
Db 233 TATGACCCCGTGTGTGTGTAGCTAACGGCTTAAGTATCCGCTGGGGAGTAGCTTGG 174
    |||
OY 878 CAAGTTAAACTCAATGAATTGACGGGGGCCCGCACAAAGCGGTGAGCATGTGTTTA 937
    |||
Db 173 CAAGATGAAGACTCAAGGAATTGACGGGGGCCCGCACAAAGCGGTGAGCATGTGTTTA 114
    |||
OY 938 ATTGAAGCAACGGGAAGACCTTACAGGCTTGTGACATGCAATGAATCTTTAGAGATA 997
    |||
Db 113 ATTGATGCAAAAGGAAGACCTTACAGGCTTGTGACATGCGCGAATCCTTTGAAGA 54
    |||
OY 998 GATTGTGCTTGGGGAACATGAGACAGGTGTGATGATGCTGTGTGCTGAGCTC 1050
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Db 53 GAGGGGTGCTTGGGAACCGCGACACAGGTGTGATGCTGTGTGCTGAGCTC 1
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Search completed: January 30, 2004, 23:43:18
Job time : 2518.83 secs

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Db      961 GGGACACCCAGCTGAAAACGGCTGTAATACCCCTAGGCTAGAGACAAAGAGAA 902
Qy      183 GACCTTCGGGCTTCGCGTATCAGATAGAGCTAGGTGAGTAGTGTGTGAGATA 242
Db      901 TCCGCGCGAG-----GAGGGGCTCGCGTGTGATTTAGTAGTGTGTGAGGCAA 855
Qy      243 TGGCTACCAAGGCGAGCATCCGTAATCTGTGTGAGAGATGATCACTGCACTGAACT 302
Db      854 TAGCTTACCAAGGCGAGTATATAGTGTGTGAGAGATGATCACTGCACTGAACT 795
Qy      303 GAGACACCGTCCAGACTCTCTACGGGAGGACAGATGGGAGATATTGGACATAGGCGAAA 362
Db      794 GAGACACCGGCCAGACTCTCTACGGGAGGACAGATGGGAGATTTTCCGCAATGGCGAAA 735
Qy      363 GCCTGATCCAGCATCCCGCGTGTGTGAGAGATCTTCCGATTTGAAAGCACTTTAAGT 422
Db      734 GCCTGACCGAGCAATGCGCGTGTGAGAGATGAGAGGCTTACCGGCTTGAACCTTTTCC 675
Qy      423 TGGAGAGAAAGGTTGATATTAATCTGCAATTTTGAAGTTACCGACAGATTAAGCAC 482
Db      674 AGAGAGAGAG-----CAATGACGATATCTGGGAGATTAAGCAT 638
Qy      483 CGGTAATCTCTGTGCCAGACCCCGGTAATACAGAGGTTGCAAGCGTTATTCGAAATTA 542
Db      637 CGGTAATCTCTGTGCCAGACCCCGGTAATACAGAGATGCAAGCGTTATTCGGAATGA 578
Qy      543 CTGGGCGTAAAGCGCGGTAGTGTGTGTTGTTAAAGTGGAAATCCCCGGGCTCAAC 602
Db      577 TTGGGCGTAAAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 518
Qy      603 CTGGAACTGCATTAACAACTGACTGACTAGATGATGATGATGATGATGATGATGATGAT 662
Db      517 CTGGACACGGGCGTGAACAACTGACTGACTGATGATGATGATGATGATGATGATGATGAT 458
Qy      663 TGTACCGGTAAATGCGGTAGATATAGAGAGAGAACACAGGCGGAGAGCGAACCACTGGA 722
Db      457 TGTACCGGTAAATGCGGTAGATATAGAGAGAGAACACACAGGCGGAGAGCACTGTGCGG 398
Qy      723 CTAAATCTGACACTGAGGTGCGAAAGGCGTGGGAGCAAGAGTTAGATACCTGCTGAG 782
Db      397 CCGACACTGACACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 338
Qy      783 TCCAGCGCGTAAAGCATGATCACTAGCCGTTGGAAGCCTTGA-GCTTTAGTGTGCGCAAC 841
Db      337 TCCAGCGCGTAAAGCATGATCACTAGCCGTTGCGATGACACCGCGTGTGCTGTACG 278
Qy      842 TAACGATTAGTTGACCGCTGGGAGATACGCGCGCGCAAGTTAAACTCAATGATGATG 901
Db      277 TAACGATTAGTTAGTATCCCGCTGGGAGATAGTTCCGCAAGATGAATCAAGGAAATG 218
Qy      902 ACCGGGCGCGGACAGAGCGTGTGAGCATGTGTGTTAATTGGAAGCAACGCGAAGAACTTT 961
Db      217 ACCGGGCGCGGACAGAGCGTGTGAGCATGTGTGTTAATTGATGCAAGGAAAGAACTTT 158
Qy      962 ACCAGGCTTGTACATCCATGAACCTTTCTAGAGATGATGATGATGATGATGATGATGAT 1021
Db      157 ACCAGGCTTGTACATCCGCGAATCCCTTTGAAAGAGAGAGGAGTGCCTTCGAGAACCGGA 98
Qy      1022 GACAGGTGCTGCATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1068
Db      97 CACAGGTGCTGCATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 51

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RESULT 15
LOCUS   BH700021/c 995 bp DNA linear GSS 20-FEB-2002
DEFINITION BOMND50TR BO_2_3_KB Brassica oleracea genomic clone BOMND50,
            genomic survey sequence.
ACCESSION BH700021
VERSION   BH700021.1 GI:18775982
KEYWORDS  GSS.
SOURCE    Brassica oleracea
ORGANISM  Brassica oleracea

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Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 995)
AUTHORS Town,C.D., Van Aken,S., Uteierback,T., Koo,H. and Fraser,C.M.
TITLE    Whole genome shotgun sequencing of Brassica oleracea
JOURNAL  Unpublished
COMMENT  Other_GSSs: BOMND50TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
FEATURES
    source
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            /organism="Brassica oleracea"
            /mol_type="genomic DNA"
            /strain="TO100DH3"
            /db_xref="taxon:3712"
            /clone="BOMND50"
            /notes="Vector: pHOsi, Site 1: BstXI; 2-3 kb sheared
            genomic DNA inserted into pHOsi using BstXI linkers"
BASE COUNT  181 a 330 c 226 g 258 t
ORIGIN
Query Match 49.7%; Score 531.6; DB 28; Length 995;
Best Local Similarity 73.0%; Pred. No. 6,8e-144;
Matches 739; Conservative 0; Mismatches 237; Indels 37; Gaps 3;
Qy      39 CATCAAGTGAAGGCGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 98
Db      977 CATCTTAACATGACATGACAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 918
Qy      99 ATGCTTGAAGATCTGCTGTGTAAGTGGAGATACGTTCCGAAACGAGACGCTAATACCGCA 158
Db      917 ACGGTGAAGACCTGCGCTGGAGGGGAAACACACTGAAACGCGCTCTAATACCCCG 858
Qy      159 TACGTCTCAAGGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 218
Db      857 TAGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 811
Qy      219 CGGATTAGTAGTGTGAGAGATAGGCTCACCAAGGCGAGCATCCGTAAGTGTCTGAG 278
Db      810 CTGATTAGTAGTGTGAGAGATAGGCTCACCAAGGCGAGCATGATGATGATGATGATGATGAT 751
Qy      279 AGATGATCAGTCACTGGAATGAGACAGGTCCAGACTCTTACAGGAGGAGAGAGAGAGAG 338
Db      750 AGATGATCAGTCACTGGAATGAGACAGGTCCAGACTCTTACAGGAGGAGAGAGAGAGAG 691
Qy      339 GGGAAATTTGAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 398
Db      690 GGGAAATTTCCGCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 631
Qy      399 TTCGATTGTAAGCACTTTAAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 458
Db      630 TACGGGTCTGAACTTTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 594
Qy      459 TGAAGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 518
Db      593 TGAAGTATCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 534
Qy      519 GGGTGAAGGTTAATGAGATTAAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 578
Db      533 GGAATGAAAGGTTATCCGAAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 474
Qy      579 GGATGAAATCCCGGGGCTCAACCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 638
Db      473 CGCGTCAAAATCCAGAGGCTCAACCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 414

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Seq primer: TR
Class: sheared ends.

FEATURES
Location/Qualifiers
1..1069

/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO100DH3"
/db_xref="taxon:3712"
/clone="BONR59"
/note="Vector: pBOS1; Site: 1; BstXI, 1.6-2 kb sheared
total DNA inserted into pBOS1 using BstXI linkers"

BASE COUNT 200 a 351 c 248 g 270 t

Query Match 50.5%; Score 540.6; DB 29; Length 1069;
Best Local Similarity 72.6%; Pred. No. 1.7e-146; Indels 48; Gaps 4;
Matches 775; Conservative 0; Mismatches 244

QY 3 CCTTGCTCAGATTGAAACGCTGGCGGAGGCTTACACATGCAAGTCGACCGGTAGAGAGA 62
DB 1048 CCTGGCTCAGATTGAAACGCTGGCGGAGGCTTACACATGCAAGTCGACCGGAGAA----- 994
QY 63 AGCTTGCTCTCTGAGCGGCGGAGCGGTGAGTAATGCTTAGAATCTCCCTGTAGT 122
DB 993 -----GTGGTGTTCAGTGGCGGAGCGGTGAGTAATGCTTAGAATCTCCCTGTAGT 940
QY 123 GGGGATTAACGTTCCGAAACGACGCTATACCGCATACGTTCTTACCGGAGAAACGAGG 182
DB 939 GGGGATTAACGTTCCGAAACGACGCTATACCGCATACGTTCTTACCGGAGAAACGAGG 880
QY 183 GACCTTCGGGCTTGGGCTATAGATGAGCCTAGTCCGATTAGTGTAGTGAAGTAA 242
DB 879 TCCGCCCGAG-----GAGGGCTCCGCTGATTAGTGTAGTGAAGTAA 833
QY 243 TGGCTCAGCAAGCGGAGATCCGTAAGTGTGAGAGATGATCAGTCACTGAACT 302
DB 832 TAGCTTACCAAGCGCATGATCAGTGTGCTGAGAGAGATGATCAGTCACTGAACT 773
QY 303 GAGACACGCTCCAGATCTCTACGAGGAGAGAGATGGGAAATATTGCAATGGCGGAA 362
DB 772 GAGACACGCTCCAGATCTCTACGAGGAGAGAGATGGGAAATATTGCGCAATGGCGGAA 713
QY 363 GCGTATCCAGCAGTCCGCTGTGTGAAGAGGCTTCGATTGTAAAGCACTTTAGT 422
DB 712 GCGTATCCAGCAGTCCGCTGTGTGAAGAGGCTTCGATTGTAAAGCACTTTAGT 653
QY 423 TGGAGGAGAGGTTGATTAATCTGCAATTTGACGTTACCGACAGATTAAGCAC 482
DB 652 AGGAGAGAG-----CAATGACGTTATCTGGGAGATTAAGCAT 616
QY 483 CGGCTAATCTGTGACAGAGCGCGGATTAATCAGAGGATGCAAGCGTTAATCGGAATTA 542
DB 615 CGGCTAATCTGTGACAGAGCGCGGATTAATCAGAGGATGCAAGCGTTAATCGGAATTA 556
QY 543 CTGGGCGTTAAGCGCGGATGAGTGTGTTAGTGAATATCCCGGGCTCAAC 602
DB 555 TTGGGCGTTAAGCGCGGATGAGTGTGTTAGTGAATATCCCGGGCTCAAC 496
QY 603 CTGGGAACTGCAATTCAAAATGATGATAGTGTGTTAGGAGGTTGGAATTTCTG 662
DB 495 CTTGAGACAGCGCGTGGAAATCTACCAAGCTTGAATGATGAGGAGCAAGGAAATTTCCG 436
QY 663 TGTAGCGGTGAATGCGGTATATAGAGAGAAACCAAGTGGGAGGCAACCACTGGA 722
DB 435 TGTAGCGGTGAATGCGGTATATAGAGAGAAACCAAGTGGGAGGCAACCACTGCGG 376
QY 723 CTATATCTGACACTGAGGTGCGAAAGCGGGGAGCAACAGATTGATTAATCCTGTAG 782
DB 375 CCGACACTGACACTGAGAGACGAAGCTTAGGGAGCAATGGATTGATTAATCCTGTAG 316
QY 783 TCCAGCGCGTTAAGCATGTCAAATGCGGTTGAAAGCTTGA-CTTTTATGTGCGGAGC 841

DB 315 TCCTAGCCGTTAAGCATGATGATTAAGGCGCTGTGCTGATGACCCCGTCACTGCTAGC 256
QY 842 TAACCATTTAAGTTGACCGCTGGGAGTACGCGCGGAGGTTAAATCTGAAATGATG 901
DB 255 TAACCATTTAAGTTGACCGCTGGGAGTACGCGCGGAGGTTAAATCTGAAATGATG 196
QY 902 ACGGGGCGCGGAGAGGCGGTGAGCATGTGTTAATGAGAGCAACGGGAGACCTT 961
DB 195 ACGGGGCGCGGAGAGGCGGTGAGCATGTGTTAATGAGAGCAACGGGAGACCTT 136
QY 962 ACCAGGCTTGAATTCATGAACTTTCTAGATGATGTTGCTTCCGGAACATTA 1021
DB 135 ACCAGGCTTGAATTCATGAACTTTCTAGATGATGTTGCTTCCGGAACATTA 76
QY 1022 GACAGTGTCTGATGCTGTGCTGAGCTGCTGTTGAAATGTTAAG 1068
DB 75 CACAGGTGTGATGCTGTGCTGAGCTGCTGTTGAAATGTTAAG 29

RESULT 14
BZ469058/c 1106 bp DNA linear GSS 13-DEC-2002
LOCUS BZ469058
DEFINITION BONHE54TF BO.1.6.2_KB_tot Brassica oleracea genomic clone BONHE54,
genomic survey sequence.
ACCESSION BZ469058
VERSION BZ469058.1 GI:26764665
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; euroside II; Brassicales; Brassicaceae; Brassica.
REFERENCE
TOWN,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished
Other GSSs: BONHE54TR
COMMENT
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org

DB 1010 -----TGTTCAGTGGCGGAGGTTGATTAACCGGTAGAACTGCTCC-CTTGA 962
QY 123 GGGGATTAACGTTCCGAAACGCTTAATACGCAATAGCTCTTACGAGGAGAAAGCAGG 182

FEATURES
Location/Qualifiers
1..1106

/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO100DH3"
/db_xref="taxon:3712"
/clone="BONHE54"
/note="Vector: pBOS1; Site: 1; BstXI, 1.6-2 kb sheared
total DNA inserted into pBOS1 using BstXI linkers"

BASE COUNT 211 a 360 c 255 g 280 t
Query Match 50.4%; Score 539.8; DB 29; Length 1106;
Best Local Similarity 73.2%; Pred. No. 2.9e-146; Indels 49; Gaps 5;
Matches 781; Conservative 0; Mismatches 237

QY 3 CCTTGCTCAGATTGAAACGCTGGCGGAGGCTTACACATGCAAGTCGACCGGTAGAGAGA 62
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QY 63 AGCTTGCTCTCTGAGCGGCGGAGCGGTGAGTAATGCTTAGAATCTGCTGTAGT 122
DB 1010 -----TGTTCAGTGGCGGAGGTTGATTAACCGGTAGAACTGCTCC-CTTGA 962
QY 123 GGGGATTAACGTTCCGAAACGCTTAATACGCAATAGCTCTTACGAGGAGAAAGCAGG 182

QY 684 TATAGAGAGAACACCGTGGCCGAGCCGACCTTGACTAATACTGACCTAGGTC 743
 DB 430 TATTGAGAGAACACCGTGGCCGAGCCGACCTTGACTAATACTGACCTAGGTC 371
 QY 744 GAAAGCTGGGAGACAAACAGATTAGATACCTGCTAGTCCACGCCGTAACGATGTC 803
 DB 370 GAAAGCTGGGAGACAAACAGATTAGATACCTGCTAGTCCACGCCGTAACGATGTC 311
 QY 804 ACTAGCCGTTGAAAGCCTTGAGCTTTAGTGGCGACGCTAACGCAATTAAGTGAACGCT 863
 DB 310 ACTAGCCGTTGAAAGCCTTGAGCTTTAGTGGCGACGCTAACGCAATTAAGTGAACGCT 251
 QY 864 GGGAGTACGGCCGACGATTAACCTCAATGATTAACGGGGCCGACAGAGGGTG 923
 DB 250 GGGAGTACGGCCGACGATTAACCTCAATGATTAACGGGGCCGACAGAGGGTG 191
 QY 924 GAGCATGTGTTTAAATGAGCAACGCGAAGACCTTACGAGCCTTGACATCCATGA 983
 DB 190 GAGCATGTGTTTAAATGAGCAACGCGAAGACCTTACGAGCCTTGACATCCATGA 131
 QY 984 ACTTCTAGAGATGATGATGCTCGGAGACATTAAGAGAGGCTGATGCTGTCG 1043
 DB 130 ACTTCTAGAGATGATGATGCTCGGAGACATTAAGAGAGGCTGATGCTGTCG 71
 QY 1044 TCAGCTCGTGTGTGAATGTAAAG 1068
 DB 70 TCAGCTCGTGTGTGAATGTAAAG 46

RESULT 12

B2558387 1072 bp DNA linear GSS 17-DEC-2002
 LOCUS pasci-60_980.s1 pasci-60 Pseudomonas aeruginosa genomic clone
 DEFINITION B2558387
 ACCESSION B2558387
 VERSION B2558387.1 GI:27172682
 KEYWORDS GSS.
 SOURCE Pseudomonas aeruginosa
 ORGANISM Pseudomonas aeruginosa
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 Pseudomonadaceae; Pseudomonas.

REFERENCE 1 (bases 1 to 1072)
 Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.F., Hastings, M.,
 Burns, J.U., Kaul, R., and Olsen, M.V.
 TITLE Whole-Genome-Sequence Variation among multiple isolates of
 Pseudomonas aeruginosa library
 JOURNAL J. Bacteriol., (2002) In press
 COMMENT Contact: Chris K. Raymond
 Genome Center
 University of Washington
 Box 352145, Seattle, WA 98105-2145, USA
 Tel: 2062216954
 Fax: 2066857244
 Email: craymond@u.washington.edu
 Class: Shotgun.

FEATURES

Location/Qualifiers
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 /organism="Pseudomonas aeruginosa"
 /mol_type="genomic DNA"
 /strain="1-60"
 /db_xref="taxon:287"
 /clone="pasci-60_980"
 /clone_1bp="pasci-60"
 /note="clinical isolate 1-60 whole genomic shotgun library."
 BASE COUNT 273 a 233 c 313 g 252 t 1 others
 ORIGIN

Query Match 51.2%; Score 548; DB 29; Length 1072;
 Best Local Similarity 88.6%; Pred. No. 1,1e-148;
 Matches 616; Conservative 0; Mismatches 76; Indels 3; Gaps 2;
 QY 3 CTTTGTCAAGATTGAACGCTGGCGGACGCTTAACATGCAATGACGCGGTAGAGAGA 62

DB 126 CATGCTCAGATTGAACGCTGGCGGAGGCTTAACATGCAATGCAATGACCGAATGAAGG 185
 QY 63 AGCTTCTTCTTGAAGACGGCGGACGGGTGAGTAAATGCTTAGGAATCTGCTGTAGT 122
 DB 186 AGCTTCTTCTTGAAGACGGCGGACGGGTGAGTAAATGCTTAGGAATCTGCTGTAGT 245
 QY 123 GGGGATTAACGTTCCGGAACCGACGCTAATACCGCATACGCTTCCAGGAGAAAGCAGG 182
 DB 246 GGGGATTAACGTTCCGGAACCGACGCTAATACCGCATACGCTTCCAGGAGAAAGTGGG 305
 QY 183 GACCTTCCGAGCCTTGGCTATCAGATGAGCTAGTCCGATTAAGCTAGTGTAGGTA 242
 DB 306 GATCTTCGACCTCAGACGCTATCAGATGAGCTAGTCCGATTAAGCTAGTGTAGGTA 365
 QY 243 TGCTTACCAAGGCGACGATCCGTAATCTGCTTGAAGATGATCAGTCACTGGAACT 302
 DB 366 AGGCTTACCAAGGCGACGATCCGTAATCTGCTTGAAGATGATCAGTCACTGGAACT 425
 QY 303 GAGACAGGTCGACCTCTTACAGGAGGACAGTGGGGAATTAATGACAAATGGGCGAA 362
 DB 426 GAGACAGGTCGACCTCTTACAGGAGGACAGTGGGGAATTAATGACAAATGGGCGAA 485
 QY 486 -CTGATCCAGCATCGCGCTGTGTGAAGAGCTTCCGATTTGAAGCACTTAAAGT 544
 DB 423 TGGAGAGAGGCTGTGATTAATCTCGCAATTTAGCTTCCGACAGATTAAGAC 482
 QY 545 TGGAGAGAGGCTGTGATTAATCTCGCAATTTAGCTTCCGACAGATTAAGAC 604
 DB 483 CGGCTACTCTGTGCCAGAGCCGCGTAATACAGAGGCTGCAAGCTTAAATCGGAATTA 542
 QY 605 CGGCTACTCTGTGCCAGAGCCGCGTAATACAGAGGCTGCAAGCTTAAATCGGAATTA 664
 DB 543 CTGGCGGTAAAGGCGCGTAAAGTGTGTTGTTAGTGTGAATATCCCGGGCTCAAC 602
 QY 665 CTGGCGGTAAAGGCGCGTAAAGTGTGTTGTTAGTGTGAATATCCCGGGCTCAAC 724
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 QY 725 CTGGGAACATGCAATTCGAACTGACTAGATGATGTAGTA--GGGTGTGGAATTTCC 784
 DB 661 TGTGTACCGGTGAATGCTTAATTTAGGAAGAA 695
 QY 785 TGTGTACCGGTGAATGCTTAATTTAGGAATTTAGGA 819

RESULT 13

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 LOCUS BONKRS59TR_BO_1.6_2_XE_tot Brassica oleracea genomic clone BONKRS59,
 DEFINITION B2474941
 ACCESSION B2474941
 VERSION B2474941.1 GI:26776372
 KEYWORDS GSS.
 SOURCE Brassica oleracea
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 1069)
 Town, C.D., Van Aken, S., Utechtack, T., Koo, H. and Fraser, C.M.
 TITLE Whole genome shotgun sequencing of Brassica oleracea
 JOURNAL Unpublished
 COMMENT Other_GSSs: BONKRS59TF
 Contact: Chris Town

TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
BF845685	559 bp	BF845685	700B5 cDNA from differential display on Platinum-treated embryos	EST.	Xenopus laevis	Xenopus laevis (African clawed frog)	Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryotes; Metazoa; Chordata; Anura; Mesobatrachia; Pipridae; Pipridae; Xenopodinae; Xenopus.	Monetti, C., Vegetti, D., Gornati, R., Prati, M. and Bernardini, G.	Platinum toxicity and gene expression in Xenopus embryos: analysis by FEMAX and differential display	Unpublished	Contact: Monetti C Department of Structural and Functional Biology University of Insubria Via Dunant 3, 21100, Varese, Italy Tel: ++39332421328 Fax: ++39332421300 Email: cmonetti@uninsubria.it. Location/Qualifiers
FEATURES	source	1. 559	/organism="Xenopus laevis"	/mol_type="mRNA"	/db_xref="taxon:8355"	/tissue_type="Whole 5-days embryos"	/clone_lib="cDNA from differential display on Platinum-treated embryos"	115 a	111 c	174 g	119 t
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Query Match	52.1%; Score 557; DB 10; Length 559;										
Best Local Similarity	100.0%; Pref. No. 1.9e-151;										
Matches 557;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;										
QY	253	AGGCGAGCATCCGTAACGTGCTGTGAGAGATGATCACTGTGACAGACCGT	312								
Db	3	AGGCGAGCATCCGTAACGTGCTGTGAGAGATGATCACTGTGACAGACCGT	62								
QY	313	CCGAGATCCTTAGGGAGGAGCAGAGCGGGGTAATTGGACATAGGGGAAAGCTTATCCA	372								
Db	63	CCGAGATCCTTAGGGAGGAGCAGAGCGGGGTAATTGGACATAGGGGAAAGCTTATCCA	122								
QY	373	GCCATGCCGCGTGTGTGAAGAGGCTCTTCGGATTGTAAGCACTTTAAGTTGGAGAG	432								
Db	123	GCCATGCCGCGTGTGTGAAGAGGCTCTTCGGATTGTAAGCACTTTAAGTTGGAGAG	182								
QY	433	GGTTTAGATTAATCTCTGCAATTTTGAAGTTTGAAGTATGACAGATTAAGCACCGGCTTA	492								
Db	183	GGTTTAGATTAATCTCTGCAATTTTGAAGTATGACAGATTAAGCACCGGCTTA	242								
QY	493	TGTGCAGAGAGCCGCGGTATACAGAGGTGCAAGCCTTAATCGAATTAATCTGCGCGTAA	552								
Db	243	TGTGCAGAGAGCCGCGGTATACAGAGGTGCAAGCCTTAATCGAATTAATCTGCGCGTAA	302								
QY	553	AGGAGCCGAGTAGGTGTTTGTTAAGTTGGATGTGAATCCCGGGGCTCAACCTGGGAAATG	612								
Db	303	AGGAGCCGAGTAGGTGTTTGTTAAGTTGGATGTGAATCCCGGGGCTCAACCTGGGAAATG	362								
QY	613	CATTCAAACTAGTACTGACTAGTATGTGTAGAGGTGTGGAATTTCTGTGTAGCGGTG	672								
Db	363	CATTCAAACTAGTACTGACTAGTATGTGTAGAGGTGTGGAATTTCTGTGTAGCGGTG	422								
QY	673	AAATGGTGTGATATAGGAAGAAACCAAGGTGCGAAGCGACCACTGTGACTTAATATCGA	732								
Db	423	AAATGGTGTGATATAGGAAGAAACCAAGGTGCGAAGCGACCACTGTGACTTAATATCGA	482								
QY	733	CACCTAGGTGTGCAAAAGCGTGGGAGCAAAACGATTATGATCCCTGTGTATGTCACGCGCT	792								

Db	483	CACGTAGAGTGGCGAAAGCGTGGGAGACAAACAGGANTTGAATACCTGGTATCCACCCCT	542
QY	793	AAACGATGTCACCTAGC	809
Db	543	AAACGATGTCACCTAGC	559
RESULT 11			
LOCUS	CD044496/c		
DEFINITION	CD044496	674 bp	mRNA
ACCESSION	CD044496		linear
VERSION	CD044496		EST 09-MAY-2000
KEYWORDS	CD044496.1	GI:30498089	
SOURCE	EST.		
ORGANISM	Phytophthora sojae		
REFERENCE	Phytophthora sojae		
AUTHORS	Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;		
TITLE	Phytophthora 1.		
JOURNAL	1 (bases 1 to 674)		
COMMENT	Tyler,B.M., Judelson,H.S., Gilzen,M., Dean,R.A. and Vaughn,M.E.		
	USDA-IPAFS: Expression of Phytophthora sojae genes during infection		
	and propagation		
	Unpublished		
	Contact: Tyler B		
	Tyler lab		
	VBI		
	1880 Pratt Dr., Blacksburg, VA 24061, USA		
	Tel: 540-231-7318		
	Email: bmtyle@vt.edu		
	PCR Primers		
	FORWARD: BK reverse		
	Primer: 014 row: K column: 10		
	Seq primer: BK reverse		
	High quality sequence stop: 674.		
FEATURES	Location/Qualifiers		
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	/tissue_type="infected host tissue"		
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	post infection"		
	/note="Vector: pBK-CMV; Site 1: EcoRI; Site 2: XhoI;		
	USDA-IPAFS: Expression of Phytophthora sojae genes during		
	infection and propagation."		
BASE COUNT	148 a 206 c 149 g 170 t	1 others	
ORIGIN			
Query Match	51.9%	Score 555.2;	DB 14; Length 674;
Best Local Similarity	93.0%	Pred. No. 7.1e-151;	
Matches 581; Conservative	0; Mismatches 44; Indels	0; Gaps	0;
QY	444	AATACCTCATTTTACGTTACCGACAGATAGACAGCGGTACTCTGTGCCAGCAG	503
Db	670	AATACCTGAGATTTTACGTTACCGACAGATAGACAGCGGTACTCTGTGCCAGCAG	611
QY	504	CCGCGGTAAATACAGAGGGGTGCAAGCGTTAATCGAATTACTGGGCGTAAAGCGCGGTAG	563
Db	610	CCGCGGTAAATACAGAGGGGTGCAAGCGTTAATCGAATTACTGGGCGTAAAGCGCGGTAG	551
QY	564	GTCGTTGTTAGTGGATGGAATGCCGGGCTCACTGCGAATCATTTCAAAAT	623
Db	550	GTCGTTGTTAGTGGATGGAATGCCGGGCTCACTGCGAATCATTTCAAAAT	491
QY	624	GACTGACTAGAGTATGATGAGGGGTGTGGAATTTCTGTGTAGCCGTAAATGCGTAGA	683
Db	490	GTCGTGCTAGAGTGGGTGAGGGGTATGGAATTTCCAGTGTAGCCGTAAATGCGTAGA	431

QY 111 CTG--CCTGGTAGTGGGGATTAACGTTTCGAAAACGAGCGCTAATACCGCATACGCTTAC 168
DB 784 TTGGCCCTTGTAATGGGAAAACGTCGAGAAACGGGCGCTAAACCGGAAACGCTCGA 725
QY 169 GGGAGAAA-GCAGGGGACCTTCGGGCTTCGCTATCAGATGAGCCTAGTCGATTAGC 227
DB 724 GGGAGAAAAGGGGGGATCTTGGGACCCACCGCTTCAATGATGAGCTAGTCGATTAGC 665
QY 228 TAAGTTGAGAGTAATAGGCTCAACCAAGGGGAGC-ATCCGTAATCTGCTGAGAGATAT 286
DB 664 AAGTTGGTGGTAAAGGCCCTCCAGGAGGAGAACTCCGTAATCTGCTTAAAGATGAT 605
QY 287 CAGTCACTGTAAGTGAAGCAGGTCAGACTCTCTACGAGGAGCAGTGGGAAATAT 346
DB 604 CAGTCACTGTAAGTGAAGCAGGTCAGACTCTCTACGAGGAGCAGTGGGAAATAT 545
QY 347 TGAACATGGGGGAAAGCCTGATCAAGCCATGCGCGTGTGTGAAGAGTCTTGGAAT 406
DB 544 TGACATATGGGCGAAAGCCTGATCCAGCATGCGCGTGTGTGAAGAGTCTTGGAAT 485
QY 407 GTAAGCACTTAAAGTTGGAGGAGGTTGATTAATTAATCTGCAATTTTGAAGTTA 466
DB 484 GTAAAGCACTTAAAGTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 425
QY 467 CGACAGATTAAGCAGCGGCTAACTCTGTCAGAGCAGCGCGGTAATACAGAGGTCGA 526
DB 424 CCAACAGATTAAGCAGCGGCTAACTCTGTCAGAGCAGCGCGGTAATACAGAGGTCGA 365
QY 527 GCGTTAATCGGAATTAATCTGGGCTAAAGGCGGTAAGTGTGTGAAGTTGAATGTA 586
DB 364 GCGTTAATCGGAATTAATCTGGGCTAAAGGCGGTAAGTGTGTGAAGTTGAATGTA 305
QY 587 AATCCCGGCTCAACCTGGGAACTGATTAATACTGATAGAGTATGAGTGAAG 646
DB 304 AATCCCGGCTCAACCTGGGAACTGATTAATACTGATAGAGTATGAGTGAAG 245
QY 647 GTGTGGAATTTCTGTGTGAAGGCTGAATTCGTGATATAGAAAGAAACACAGTGGC 706
DB 244 GTGTGGAATTTCTGTGTGAAGGCTGAATTCGTGATATAGAAAGAAACACAGTGGC 185
QY 707 AAGGCGACCACTGAGCTAATTAATGACACTGAGGTGCAAGCGTGGGAGCAACAGGA 766
DB 184 AAGGCGACCACTGAGCTAATTAATGACACTGAGGTGCAAGCGTGGGAGCAACAGGA 125
QY 767 TTGATTAACCTGTGATGCAAGCGGTAACGATGTCATGAGCCGTTGGAAGCTTGAAC 826
DB 124 CTGATTAACCTGTGATGCAAGCGGTAACGATGTCATGAGCCGTTGGAAGCTTGAAC 65

RESULT 9
CD043647/c 699 bp mRNA linear EST 09-MAY-2003
LOCUS JSHB009XK05f_180500 JSHB. Infected hypocotyl soybean host. 48 hrs
DEFINITION post infection Phytophthora sojae cdna clone JSHB009X05 5, mRNA
sequence.
CD043647
VERSION CD043647.1 GI:30497240
KEYWORDS EST.
SOURCE Phytophthora sojae
ORGANISM Phytophthora sojae
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
Phytophthora.
REFERENCE 1. (bases 1 to 699)
Tyler B.M., Jungelson H.S., Gijzen M., Dean R.A. and Waugh M.E.
TITLE USDA-IPAFS: Expression of Phytophthora sojae genes during infection
and propagation
JOURNAL Unpublished
COMMENT Contact: Tyler B
Tyler lab
VBI
1880 Pratt Dr., Blackeburg, VA 24061, USA
Tel: 540-231-7318

Email: bmyler@vt.edu
PCR Primers
FORWARD: BK reverse
Reverse: BK reverse
Plates: 009 row: K column: 05
Seq primer: BK reverse
High quality sequence stop: 699.
Location/Qualifiers
1. 699
/organism="Phytophthora sojae"
/mol_type="mRNA"
/db_xref="taxon:67593"
/clone="JSHB009X05"
/tissue_type="infected host tissue"
/cell_line="P6497"
/dev_stage="48 hour post infection"
/clone_lib="JSHB: Infected hypocotyl soybean host. 48 hrs
post infection"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI;
USDA-IPAFS: Expression of Phytophthora sojae genes during
infection and propagation."
BASE COUNT 153 a 212 c 156 g 178 t
ORIGIN
Query Match 52.2%; Score 559; DB 14; Length 699;
Best Local Similarity 92.2%; Pred. No. 5.6e-15;
Matches 589; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 430 AAGGTTGATGATTAATCTGCAATTTTGAAGTTCAGACAGATTAAGCAGCGCTAA 489
DB 699 AAGGTTTACAGCAATACCTGTGATTTTACGTTACGACAGATTAAGCAGCGCTAA 640
QY 490 CTCTGTGCAAGAGCCCGGCTAATACAGAGGTCGACGCTTAATCGGAATTAATCGGCG 549
DB 639 CTCTGTGCAAGAGCCCGGCTAATACAGAGGTCGACGCTTAATCGGAATTAATCGGCG 580
QY 550 TAAAGCGCGTAGGAGTGTGTGTTGATGATGTAATCCCGGCTCAACCTGGGAA 609
DB 579 TAAAGCGCGTAGGAGTGTGTGTTGATGATGTAATCCCGGCTCAACCTGGGAA 520
QY 610 CTGCAATCAAACTGACTGATGATGATGATGATGATGATGATGATGATGATGATG 669
DB 519 CTGCAATCAAACTGACTGATGATGATGATGATGATGATGATGATGATGATGATG 460
QY 670 GTGAATGCGTGAATATAGAAAGCAACAGAGGCGGAGGAGGAGGAGGAGGAGGAGG 729
DB 459 GTGAATGCGTGAATATAGAAAGCAACAGAGGCGGAGGAGGAGGAGGAGGAGGAGG 400
QY 730 TGACACTGAGTGCAGAAAGCGTGGGAGCAACAGATTAATACCTGTGATGCAAGC 789
DB 399 TGACACTGAGTGCAGAAAGCGTGGGAGCAACAGATTAATACCTGTGATGCAAGC 340
QY 790 CGTAAACGATGCACTAGCCGTTGGAAGCCTTGAAGCTTGAAGTGGGCGAGCTAACCAT 849
DB 339 CGTAAACGATGCACTAGCCGTTGGAAGCCTTGAAGCTTGAAGTGGGCGAGCTAACCAT 280
QY 850 TAAAGTTGACCGGCTGGGAGTACGGGCCCAAGGTTAAATCAATGATGAGCGGGGC 909
DB 279 TAAAGTTGACCGGCTGGGAGTACGGGCCCAAGGTTAAATCAATGATGAGCGGGGC 220
QY 910 CCGCAGACCGGTGAGAGCATGTGTTTAATCGAAGCAACCGGAAGAACTTACAGGCC 969
DB 219 CCGCAGACCGGTGAGAGCATGTGTTTAATCGAAGCAACCGGAAGAACTTACAGGCC 160
QY 970 TTGACATCAATGAATCTTCTAGAGATGATGATGATGATGATGATGATGATGATGATG 1029
DB 159 TTGACATCAATGAATCTTCTAGAGATGATGATGATGATGATGATGATGATGATGATG 100
QY 1030 CTGCAATGCTGTGCTGACGCTGTGTGTGAATGTAAG 1068
DB 99 CTGCAATGCTGTGCTGACGCTGTGTGTGAATGTAAG 61

RESULT 10

QY 894 ATGA 897
 DB 601 ATGA 604

RESULT 7
 LOCUS CD040169/c 641 bp mRNA linear EST 09-MAY-2003
 DEFINITION psfH032xK20f.293343 psfH: Infected hypocotyl soybean host. 48 hrs post infection Phytophthora sojae cDNA clone sHB032K20 5, mRNA sequence.

ACCESSION CD040169
 VERSION CD040169.1 GI:30502041
 KEYWORDS EST
 SOURCE Phytophthora sojae
 ORGANISM Phytophthora sojae
 Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae; Phytophthora.

REFERENCE 1 (bases 1 to 641)
 Tyler B.M., Judelson H.S., Gijzen M., Dean R.A. and Maugh M.B. USDA-IRAFs: Expression of Phytophthora sojae genes during infection and propagation
 Unpublished
 Contact: Tyler B
 Tyler lab
 VBI
 1860 Pratt Dr., Blacksburg, VA 24061, USA
 Tel: 540-231-7318
 Email: bmtyle@vt.edu

PCR PRIMERs
 FORWARD: BK reverse
 Plate: 032 row: K column: 20
 Seq primer: BK reverse

FEATURES
 High quality sequence stop: 641.
 Location/Qualifiers
 1..641
 /organism="Phytophthora sojae"
 /mol_type="mRNA"
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 /cell_line="p6497"
 /dev_stage="48 hour post infection"
 /clone_id="psfH: Infected hypocotyl soybean host. 48 hrs post infection"
 /note="Vector: pBK-CMV; Site 1: EcoRI; Site 2: XhoI; USDA-IRAFs: Expression of Phytophthora sojae genes during infection and propagation."
 BASE COUNT 135 a 199 c 142 g 164 t 1 others

ORIGIN
 Query Match 52.9%; Score 566.4; DB 14; Length 641;
 Best Local Similarity 96.3%; Pred. No. 3.7e-154;
 Matches 579; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 468 CGACGATTAAGACCGGCTACTCTGTCGACGACCGGCGTAATACAGAGGCTCAAG 527
 DB 641 CGACGATTAAGACCGGCTACTCTGTCGACGACCGGCGTAATACAGAGGCTCAAG 582

QY 528 CGTTAATCGAATTAAGGCGGTAAGCGCGCGTAAGGCGTTGTTGAATGAGTGA 587
 DB 581 CGTTAATCGAATTAAGGCGGTAAGCGCGCGTAAGGCGTTGTTGAATGAGTGA 522

QY 588 ATCCCGGCGCTCAACCTGCGAAGCTGCATTCATAAATCTAGTATAGTGAAGG 647
 DB 521 ATCCCGGCGCTCAACCTGCGAAGCTGCATTCATAAATCTAGTATAGTGAAGG 462

QY 648 TGGTGAATTTCTGTAGCGGTGAATGCGGTATAGTGAAGAACCAAGTGGCA 707
 DB 461 TGGTGAATTTCTGTAGCGGTGAATGCGGTATAGTGAAGAACCAAGTGGCA 402

QY 708 AGGGACCACTGACATTAATCTACACTGAGGTGCGAAAGCGTGGGAGCAACCGAT 767

DB 401 AGCGAACCACTGACCTGATTAATCTGACACTGAGGTGCGAAAGCGTGGGAGCAACAGAT 342

QY 768 TAGATACCTGTGTAGTCAAGCGCGTAATACATGATGCACTAGGCGTTGGAAGCTTGAGCT 827
 DB 341 TAGATACCTGTGTAGTCAAGCGCGTAATACATGATGCACTAGGCGTTGGAAGCTTGAGCT 282

QY 828 TTTAGTGGCGGCACTAAGCATTAAGTTAAGCCCTGGGGAGTACGGCGCAAGTTAA 887
 DB 281 CTTAGTGGCGGCACTAAGCATTAAGTTAAGCCCTGGGGAGTACGGCGCAAGTTAA 222

QY 888 ACTCAATGATTAAGCGGGGCGCGCACAAGCGGTGAGCATGTGTTAAATTCGAAACA 947
 DB 221 ACTCAATGATTAAGCGGGGCGCGCACAAGCGGTGAGCATGTGTTAAATTCGAAACA 162

QY 948 ACGGGAAGACCTTACCAAGCGCTTGCATCCATGAATCTTTAAGATAGATTGTTGCC 1007
 DB 161 ACGGGAAGACCTTACCAAGCGCTTGCATCCATGAATCTTTAAGATAGATTGTTGCC 102

QY 1008 TTGGGAACATTAAGACAGAGTGTGATGCTGTGATGCTGTGATGCTGTGATGCTGTGATG 1067
 DB 101 TTGGGAACATTAAGACAGAGTGTGATGCTGTGATGCTGTGATGCTGTGATGCTGTGATG 42

QY 1068 G 1068
 DB 41 G 41

RESULT 8
 B2561605/c 1033 bp DNA linear GSS 17-DEC-2002
 LOCUS pacs2-164_3345.y2 pacs2-164 Pseudomonas aeruginosa genomic clone
 DEFINITION pacs2-164_3345, genomic survey sequence.

ACCESSION B2561605
 VERSION B2561605.1 GI:27181948
 KEYWORDS GSS.

SOURCE
 ORGANISM Pseudomonas aeruginosa
 Pseudomonas aeruginosa
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.

REFERENCE 1 (bases 1 to 1033)
 Spencer D.H., Raymond C.K., Smith E.E., Sims E.E., Hastings M., Burns J.L., Kaul R. and Olsen M.V. Whole-Genome-Sequence variation among multiple isolates of Pseudomonas aeruginosa library J. Bacteriol. (2002) in press

JOURNAL
 CONTACT: Chris K. Raymond
 Genome Center
 University of Washington
 Box 352145, Seattle, WA 98105-2145, USA
 Tel: 2062216954
 Fax: 2066857244
 Email: craymond@u.washington.edu

FEATURES
 Class: Shotgun.
 Location/Qualifiers
 1..1033
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 /script="2-164"
 /db_xref="taxon:287"
 /clone="pacs2-164_3345"
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 /note="Clinical isolate 2-164 Whole genomic shotgun library."

BASE COUNT 216 a 313 c 223 g 280 t 1 others

ORIGIN
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 Best Local Similarity 85.3%; Pred. No. 4.8e-154;
 Matches 665; Conservative 0; Mismatches 111; Indels 4; Gaps 3;

QY 51 GCGGTAGAGAGAGCTTCTCTCTTCTGAGAGCGGCGGAGTATGCTAGAT 110
 DB 844 GAGATGAAGGAACTTCTCTCTGATTCACCGCGGAGCGGTGAGTATTCCTAGAA 785

DEFINITION 3B5 cDNA library of 4-day-old *Eucalyptus globulus* bicostata-Pisolithus tinctorius ectomycorrhiza Pisolithus tinctorius cDNA 5' similar to PMN-binding protein, mRNA sequence.

ACCESSION AM600903

VERSION AM600903.1 GI:7304774

KEYWORDS EST

SOURCE Pisolithus tinctorius

ORGANISM Pisolithus tinctorius
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes; Boletales; Sclerotidiales; Pisolithaceae; Pisolithus.

REFERENCE 1 (bases 1 to 660)
Voibret, C., Duplessis, S., Encelot, N. and Martin, F.
Identification of symbiosis-regulated genes in *Eucalyptus globulus*-*Pisolithus tinctorius* ectomycorrhiza by differential hybridization of arrayed cDNAs

JOURNAL Plant J. 25 (2), 181-191 (2001)

MEDLINE 21097016

PUBMED 11169194

COMMENT Contact: Martin FM
Equipe de Microbiologie Forestiere
Institut National de la Recherche Agronomique
Centre INRA de Nancy, 54280 Champenoux, France
Tel: +33 383 39 40 80
Fax: +33 383 39 40 69
Email: fmartin@nancy.inra.fr
Insert Length: 660 Std Error: 0.00
Seq primer: Capfinder 5/CDS
POLY=A=No.

FEATURES

source

1..660
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/db_xref="taxon:37468"
/issue_type="mantle and Hartig net hyphae"
/dev_stage="symbiotic, 4 days after contact"
/lab_host="Eucalyptus globulus bicostata"
/clone_id="cDNA library of 4-day-old *Eucalyptus globulus* bicostata-Pisolithus tinctorius ectomycorrhiza"
/note="Organ: ectomycorrhiza; Vector: pBluescript; Site: 1; EcoRI: The cDNA library was constructed from 1 ug total ectomycorrhiza RNA using the SMART cDNA library construction kit (#K10511, Clontech, Palo Alto, CA, USA) according to the manufacturer's instructions. cDNAs were cloned into EcoRI-digested pBluescript."

BASE COUNT 179 a 139 c 200 g 142 t

ORIGIN

Query Match 54.3%; Score 581; DB 9; Length 660;
Best Local Similarity 95.1%; Pred. No. 2e-158;
Matches 621; Conservative 0; Mismatches 30; Indels 2; Gaps 2;

QY 409 AAAGCATTGAAGTGGAGGAGGAGGTTGATTAATTAATCTGCAATTTTGACGTTACC 468
DB 10 AAAGCATTGAAGTGGAGGAGGAGGATTAATTAATTAATCTGCTGCTGACGTTACC 69

QY 469 GACAGATTAAGCAGCGGCTAACTCTGTGTCCAGACGCCGGTATACAGAGGCGCAAGC 528
DB 70 GACAGATTAAGCAGCGGCTAACTCTGTGTCCAGACGCCGGTATTAACAGAGGCGCAAGC 129

QY 529 GTTAATCGAATTAAGTGGAGGAGGAGGCGGCTGATGTTGTTAATGATGATGATAA 588
DB 130 GTTAATCGAATTAAGTGGAGGAGGAGGCGGCTGATGTTGTTAATGATGATGATAA 169

QY 589 TCCCGGGCTCAACTGGGAGTCAATTCATAAAGTCACTAGATATGATGAGAGGT 648
DB 190 TCCCGGGCTCAACTGGGAGTCAATTCATAAAGTCACTAGATATGATGAGAGGT 249

QY 649 GGTGAATTTCTGTGTAGCGGTGAATGCGTAGATATAGAGAGGACACACAGCGCGGAA 708
DB 250 AGTGAATTTCTGTGTAGCGGTGAATGCGTAGATATAGAGAGGACACACAGCGCGGAA 309

QY 709 GGGAGCACCCTGGAATTAATTAATGACATGAGGTGCGAAAGCGTGGGAGACAAACAGGATT 768

DB 310 GGGAGCACCCTGGAATTAATTAATGACATGAGGTGCGAAAGCGTGGGAGACAAACAGGATT 369

QY 769 AGATACCTGTGTAGTCCAGCCCGTAAACGATGTCATTAAGCCGTTGGAAGCCTTGAGCTT 828

DB 370 AGATACCTGTGTAGTCCAGCCCGTAAACGATGTCATTAAGCCGTTGGAAGTCTGTGACATC 429

QY 829 TTAGTGGGCGACGCTTAACGATTAAGTGAACCCCTGGGAGATACGCCCGCAAGTTTAAA 888

DB 430 TTAGTGGGCGACGCTTAACGATTAAGTGAACCCCTGGGAGATACGCCCGCAAGTTTAAA 489

QY 889 CTCAATTAATTAAGCGGCGCGCCGACCAAGCGGTGAGCATGTGTTAATGAGAGCA 948

DB 430 CTCAATTAATTAAGCGGCGCGCCGACCAAGCGGTGAGCATGTGTTAATGAGAGCA 548

QY 949 CGCGAAGACCTTACACAGGCGCTTACATCCATGAATGAACTTTTGAAGATATGATGTCCT 1008

DB 549 CGCGAAGACCTTACACAGGCGCTTACATCCATGAATGAACTTTTGAAGATATGATGTCCT 608

QY 1009 TCGGGAACATTAAGACAGGCGGTGCGATGCGTGTGTCAGTGTGTTGAAA 1061

DB 609 TCGGGAACATTAAGACAGGCGGTGCGATGCGTGTGTCAGTGTGTTGAAA 660

RESULT 5
BE636524 650 bp mRNA linear EST 25-AUG-2000
LOCUS SMOVL2C8A17H03SK Onchocerca volvulus L2 larvae cDNA (SAM98MLW-OVL2)
DEFINITION Onchocerca volvulus cDNA clone SMOVL2C8A17H03 5', mRNA sequence.

ACCESSION BE636524

VERSION BE636524.1 GI:9919635

KEYWORDS EST.

SOURCE Onchocerca volvulus

ORGANISM Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidae; Onchocercidae; Onchocerca.

REFERENCE 1 (bases 1 to 650)
Williams, S.A.
Genes expressed in L2 larvae of *Onchocerca volvulus*

AUTHORS Unpublished

TITLE Contact: Steven A. Williams

JOURNAL Molecular Parasitology

COMMENT Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith College, Northampton, MA, 01063, USA
Tel: 413/5853826
Fax: 413/5853786
Email: genome@smith.edu
Seq primer: pBluescript SK.

FEATURES

source

1..650
/organism="Onchocerca volvulus"
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/db_xref="taxon:6282"
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/lab_host="X11-Blue MRF"
/clone_id="Onchocerca volvulus L2 larvae cDNA (SAM98MLW-OVL2)"
/note="Vector: Lambda Uni-ZAP XR; Site: 1; Eco RI; Site: 2; Xho I; Filarial nematode parasite of humans. mRNA was prepared from approximately 9,000 L2s isolated from infected mosquitoes from Kumba, Cameroon and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 7.3 x 10⁶ independent recombinants and the average insert size is approximately 1kb. The library was constructed by Michelle Lizotte-Waniewski. The library is available from Dr. S.A. Williams, email: genome@smith.edu."

BASE COUNT 169 a 135 c 204 g 141 t 1 others

ORIGIN

Query Match 53.4%; Score 571.8; DB 10; Length 650;

QY	CTAAATCTACACTAGGTGCGAAAGCTGGGAGCAAAACAGATTAGATACCTCGTAG	782
Db	CTGACACTGACACTAGGTGGGAAAGCGTGGGAGCAAAACAGATTAGATACCTCGTAG	323
QY	TCACGCGCTTAACGATGTCACTAGCCCTTGAAAGCCTTGAGCTTTTAGTGGCCACT	842
Db	TCACGCGCTTAACGATGTCACTAGCCGTTGGGATCTTTGAGATTATGATGGCCACT	263
QY	AACGACTTAAGTTGACCGCTGGGGAGTACCGCCGCAAGTTTAAACTCAATGATTTGA	902
Db	AACGACTTAAGTTGACCGCTGGGGAGTACCGCCGCAAGTTTAAACTCAATGATTTGA	203
QY	CGGGGGCCCGGCAAAAGCGGTGAGCATGTGTTTAATTCGAAGCAACGGGAAGACCTTA	962
Db	CGGGGGCCCGGCAAAAGCGGTGAGCATGTGTTTAATTCGAAGCAACGGGAAGACCTTA	143
QY	CCAGGCGCTTGACATCCAAATGAATCTTCTAGATATGATTTGTCCTTCGGGAACATTGAG	1022
Db	CCGAGCGCTTGACATGCTGGAACCTTCCAGAGATGATTTGTCCTTCGGGAACCTAGAC	83
QY	ACAGGTGCTGACATGAGCTGTGTCAGCTGATTTGTAATGTTAAG	1068
Db	ACAGGTGCTGACATGAGCTGTGTCAGCTGATTTGTAATGTTGCG	37

RESULT	3
LOCUS	BH771024
DEFINITION	BH771024 6499 bp DNA linear GSS 01-MAY-2002
ACCESSION	F08363 Random Sequence Trg Library Lactococcus lactis
VERSION	BH771024 subsp. cremoris genomic, genomic survey sequence.
KEYWORDS	BH771024 BH771024.1 GI:20373981
SOURCE	GSS.
ORGANISM	Lactococcus lactis subsp. cremoris Lactococcus lactis subsp. cremoris

REFERENCE	1 (bases 1 to 6499)
AUTHORS	Bolotin A., Ehrlich S. D. and Sorokin A.
TITLE	Studies of genomes of dairy bacteria <i>Lactococcus lactis</i>
JOURNAL	Sci. Aliments, (2002) In press
COMMENT	Contact: Sorokin A

CRJ INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France
Tel: 33 1 34 65 25 16
Fax: 33 1 34 65 25 21
Email: sorokine@jouy.inra.fr
best homologe in strain IL1403 is ywga (78%)
Class: shotgun
High quality sequence start: 30
High quality sequence stop: 6471.
Location/Qualifiers
1..6499
FEATURES
source

```

/organism="Lactococcus lactis subsp. cremoris"
/mol_type="genomic DNA"
/strain="MG1363"
/db_xref="taxon:1359"
/clone_id="MG1363 Random Sequence Tag Library"
/notes="Vector: pSGM2; Site 1: SmaI; Library of
chromosomal fragments of L lactis strain MG1363 was
prepared by partial AluI digestion or by sonication."
BASE COUNT      1946 a      1228 c      1683 g      1642 t
ORIGIN

```

Query Match	55.3%	Score 591.4;	DB 28;	Length 6499;
Best Local Similarity	75.0%	Pred. No. 6.4e-161;		
Matches 809; Conservative	0;	Mismatches 256;	Indels 14;	Gaps 5;

Dy 3 CCTTGTGAGATTGAACGGCTGGCGGCAGCCTTAACAATGCCAAGTCGAGCGGTGAGAAGA 62
Db 542 CCTTGCTCAGAGACGAACGGCTGGCGGCCTTAACTATCAATGCAAGTTGAGCGCATGAGAATT 601

OY	63	AGCTTG----	CTTCTCTTGGAGGGGGGAGCGGGTGAAGTAAAGCTTA--GGATCTGGCTG	117
Db	602	GGGCGCTGGACCAATTGTAAGAGAGGAA	CGGGTGAATACCGCTGGGGAAATCGCTT	661
OY	118	GTATGCGGGGATTAACGTTCCGAAACGGACGCTAATCCGCATACGCTCT-----ACGG	170	
Db	662	TGAGCGGGGGACAAATTTGGAAACGAATGCTAATACCGCATATTAACCTTTAAACATPAG	721	
OY	171	GAGAAAGCAGGGGACCTTTCGGGCTTGCCTATCAGATAGCCTAGGTCGGATTAGCTAG	230	
Db	722	TTTTAAGTTGAAGATGGCAATTGGCATCTCAATGATATGATCCGCGTTGTAATTAGCTAG	781	
OY	231	TTGGTAGGTAATGAGCTCACCAGGGGACGATTCCTAATCTGCTCGAAGCATATGATCACT	290	
Db	782	TTGGTAGGTAATGAGCTCACCAGGGGACGATATCAGATAGCCTCGAAGGAGGTATGAGC	841	
OY	291	CAACTGGAACTGACACACGAGCTCCAGACTCCTACGGGAGGACGACGAGTGGGAAATTGGA	350	
Db	842	CACATTGGGACCTGAGACACGCGCCAACTCTTCGGGAGGACGACGATGGGAACTTTCG	901	
OY	351	CAATGGCGAAAGCCTGATCCAGCCATCCCGCTGTGTGAAGAAGGCTCTTCGATTGTA	410	
Db	902	CAATGACCAAAAGCTGTGACCGACACGCGCGCTGTGTGAAGAAGGTTTTCGATCTGTA	961	
OY	411	AGCACTTAAAGTGGGAAGAGGGTGT--AGATTATACTCGCAATTTGACGTTACCG	469	
Db	962	AACTCTGTTGGTAGGAAGAAAGCTTGGTAGATGGAAGAGCTCATCAAGTACGCTAACT	1021	
OY	470	ACAGATAAGACCGGGCTAACTCTGTGCCAGACCCGCGTAATACAGAGGTGCAAACG	529	
Db	1022	ACCCAAAGAGGACCGGCTAACTAGTGCACGACGCGCGGTAAATCGTAGGCTCCGACG	1081	
OY	530	TTAAATCGGAATTAAGCGGCGTAAAGCGCGGTAGGTGTTGTTAGTTGAGATGTAAT	589	
Db	1082	TTGTCCGGATTATTTGGCGGTAAAGCGACGCGAGGTGTTTATTAAAGTCTGATGAAG	1141	
OY	590	CCCCGGGCTCAACCTGGAGACTGCATTCAAACTGACTAGTAGATGTGTAGAGGTG	649	
Db	1142	GCAGTGGCTCAACCTTTGTA--TGATTTGAAACCTGGTTAAGCTTGTAGTGCAGAGAGGA	1200	
OY	650	GTGGAAATTTCCCTGTGTACGGGTGAATAGCTAATATAGGAAGAAACCAAGTGGCGAG	709	
Db	1201	GTGGAAATTCATGTGTACGGGTGAATAGCTAATATATAGGAAGAAACCGGTGGCAA	1260	
OY	710	GCAGACCACTGGAATTAATCTGACACTGAGGTGCGAAAGCGTGGGAGCAACAGATTA	769	
Db	1261	GGGCGCTCTGGCTGTAACTGACACCTGAGGCTCGAAAGCGTGGGAGCAACAGATTA	1320	
OY	770	GATACCTCTGTAGTCCACCGCGTAAAGATGTCACTAGCCGTGGAAACCTTGAGCTT	829	
Db	1321	GATACCTCTGTAGTCCACCGCGTAAAGATGTGTAGTGTGAATGATTAAGTCTT	1380	
OY	830	TAGTGGCGAGCTTAACGATTAAGTTAGCGCTGGGAGATACGCGCGCAGGTTAAAC	889	
Db	1381	CTGTATCGCAGCTTAACGATTAAGCTCGGCTGGGAGATAGACCGCAAGTTGAAC	1440	
OY	890	TCAATGAATTGAACGGGGCCCCGACAAAGCGGTGAGCATGTGGTTTATTGGAGCAAC	949	
Db	1441	TCAAAAGAAATTGACGGGGCCCCGACAAAGCGGTGAGCATGTGGTTTATTGGAGCAAC	1500	
OY	950	GCAAGAAACCTTACACGAGCTTGAATCTCAATGAATCTTGTAGAGTAAGTGTGCTT	1009	
Db	1501	GCAAGAAACCTTACACGAGCTTGAATCTGTGTGCTATTTCTAGAGATGAAAGTTCTT	1560	
OY	1010	CGGAAACATTGAGACAGGTCTGCAATGGCTGTGTCAAGCTCGTGTGTTGAATGTAAAG	1068	
Db	1561	CGGAAACCGGAAATACAGGTGTGCAATGGTGTGTCAAGCTCGTGTGTTGAATGTGAG	1619	

RESULT 4	AM600903	LOCUS	AM600903	660 bp	mRNA	Linear	EST 23-MAR-2000


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/strain="MSH"
/db_xref="taxon:287"
/clone="msh2.2610"
/clone_lib="msh"
/notes="Environmental isolate. Whole genomic shotgun
library."
BASE COUNT      241 a      203 c      284 g      175 t      2 others
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Query Match      59.0%; Score 631; DB 29; Length 905;
Best Local Similarity 89.9%; Pred. No. 6.1e-173;
Matches 731; Conservative 0; Mismatches 77; Indels 5; Gaps 5;
3 CCTGCTCAGATTGAAACCTGCGCGAGGCTTAACATGCAAGTCGAGCGGTAGAGAG 62
94 CATGGCTCAGATTGAAACCTGCGCGAGGCTTAACATGCAAGTCGAGCGGTAGAGAG 153
63 AGCTTGCTTCTCTTGAAGCGGCGAGGCTGAGTAAATGCTAGAAATCTGCTGGTAGT 122
154 AGCTTGCTTCTCTTGAAGCGGCGAGGCTGAGTAAATGCTAGAAATCTGCTGGTAGT 213
123 GGGGAGTAAACGTTGGAAACGAGCGCTAATACCGCATACGCTTACCGGAGAAAGCAGAG 182
214 GGGGAGTAAACGTTGGAAACGAGCGCTAATACCGCATACGCTTACCGGAGAAAGTGGGG 273
183 GACCTTGCGGCTTGGCGCTATCAATAGAGCTAGTGGATTGAGTGGTGGTAGAGTAA 242
274 GATCTTGAGACTCAAGCTATCAATAGAGCTAGTGGATTGAGTGGTGGTAGAGTAA 333
243 TGGCTCACCAGGCGAGCGATCCGTAATGCTGCTGAGAGATGATCACTGACATGTAAGT 302
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303 GAGACAGCGTCCAGACTCTTACGAGGAGCAGCACTGGGAAATATTGACAAATGGCGAAA 362
394 GAGACAGCGTCCAGACTCTTACGAGGAGCAGCACTGGGAAATATTGACAAATGGCGAAA 453
363 GCGTATCCAGCATGCGCGTGTGTGAAGAGTCTTGGATTGTAAAGCACTTTAAAGT 422
454 GCGTATCCAGCATGCGCGTGTGTGAAGAGTCTTGGATTGTAAAGCACTTTAAAGT 513
423 TGGAGAGAGGTTGTAGATTAAATCTCTGCAATTTTACGTTACCGACAAATTAAGCAC 482
514 TGGAGAGAGGTTGTAGATTAAATCTCTGCAATTTTACGTTACCGACAAATTAAGCAC 573
483 CGGCTAATCTGTGCAGAGCGCGGTAATACAGAGGTTGCAAGGCTTAATGGAATTA 542
574 CGGCTAATCTGTGCAGAGCGCGGTAATACAGAGGTTGCAAGGCTTAATGGAATTA 633
543 CTGGGCGTAAAGCGCGCTAGTGGTTT-GTTAAGTTGATGTGAAATCCCGGCGTCAA 601
634 CTGGGCGTAAAGCGCGCTAGTGGTTT-GTTAAGTTGATGTGAAATCCCGGCGTCAA 693
602 CTGGGCGTAAAGCGCGCTAGTGGTTT-GTTAAGTTGATGTGAAATCCCGGCGTCAA 660
694 CTGGGCGTAAAGCGCGCTAGTGGTTT-GTTAAGTTGATGTGAAATCCCGGCGTCAA 753
661 TGTGTAGCGGTGAAATGCGTAGATATAGAA-GGACACCAATGCGGAGCCACACCT 719
754 TGTGTAGCGGTGAAATGCGTAGATATAGAA-GGACACCAATGCGGAGCCACACCT 813
720 GAGCTAATATGACATGAGGT-GCGAAAGGTTGGGAGCAACAGATTAGTACCTCG 778
814 GAGCTAATATGACATGAGGT-GCGAAAGGTTGGGAGCAACAGATTAGTACCTCG 873
779 GTAGTCAAGCGCGTAAAGCATGTGACATAGCCG 811
874 GTAGTCAAGCGCG-AAAACCATGTCCATTAACCG 905

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RESULT 2
CD042372/c      741 bp      mRNA      linear      EST 09-MAY-2003
LOCUS          pSHB040F24F.302263 pSHB: Infected hypocotyl soybean host. 48 hrs
DEFINITION     post infection Phytophthora sojae cDNA clone SHB040F24 5, mRNA
sequence.
ACCESSION      CD042372.1 GI:30495965
VERSION        CD042372.1
KEYWORDS       EST.
SOURCE         Phytophthora sojae
ORGANISM       Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
Phytophthora.
REFERENCE      1 (bases 1 to 741)
AUTHORS       Tyler B.M., Judeelson, H.S., Gijzen, M., Dean, R.A. and Waugh, M.E.
TITLE         USDA-IFARS: Expression of phytophthora sojae genes during infection
              and propagation
JOURNAL        Unpublished
COMMENT        Contact: Tyler B
              VBI
              1880 Pratt Dr., Blackeburg, VA 24061, USA
              Tel.: 540-231-7318
              Email: dmtylerevt.edu
PCR PRIMERS   FORWARD: BK reverse
              Plate: 040 row: F column: 24
              Seg primer: BK reverse
              High quality sequence stop: 741.
              Location/Qualifiers
FEATURES
source
1. .741
/organism="Phytophthora sojae"
/mol_type="mRNA"
/db_xref="taxon:67593"
/clone="SHB040F24"
/tissue_type="infected host tissue"
/dev_stage="48 hour post infection"
/clone_lib="pSHB: Infected hypocotyl soybean host. 48 hrs
post infection"
/notes="Vector: PBK-CMV; Site 1: EcoRI; Site 2: XhoI;
USDA-IFARS: Expression of Phytophthora sojae genes during
infection and propagation."
BASE COUNT      159 a      230 c      164 g      187 t      1 others
ORIGIN
Query Match      56.7%; Score 606.6; DB 14; Length 741;
Best Local Similarity 92.1%; Pred. No. 7.3e-166;
Matches 650; Conservative 0; Mismatches 55; Indels 1; Gaps 1;
363 GCGTATCCAGCATGCGCGTGTGTGAAGAGTCTTGGATTGTAAAGCACTTTAAAGT 422
741 GCGTATCCAGCATGCGCGTGTGTGAAGAGGCGCTGCGTGTAAAGCACTTTAAAG- 683
423 TGGAGAGAGGTTGTAGATTAAATCTCTGCAATTTTACGTTACCGACAGATTAAGCAC 482
682 TGGAGAGAGGCTTACAGGATTAACCTGTGAGTTTGAACGTTACCGACAGATTAAGCAC 623
483 CGGCTAATCTGTGCAGAGCGCGGCTAATACAGAGGTTGCAAGGCTTAATCGGAATTA 542
622 CGGCTAATCTGTGCAGAGCGCGGCTAATACAGAGGTTGCAAGGCTTAATCGGAATTA 563
543 CTGGGCGTAAAGCGCGGTAGTGGTTTGTAAAGTTGATGTGAAATCCCGGCGTCAAC 602
562 CTGGGCGTAAAGCGCGGTAGTGGTTTGTAAAGTTGATGTGAAATCCCGGCGTCAAC 503
603 CTGGGCGTAAAGCGCGGTAGTGGTTTGTAAAGTTGATGTGAAATCCCGGCGTCAAC 662
502 CTGGGCGTAAAGCGCGGTAGTGGTTTGTAAAGTTGATGTGAAATCCCGGCGTCAAC 443
663 TGTAGCGGTAATGCGTGAATATGAGAGGAACACCGTGGCGAAGCGGACCACTCGA 722
442 TGTAGCGGTAATGCGTGAATATGAGAGGAACACCGTGGCGAAGCGGACCACTCGA 383

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 30, 2004, 18:26:40 ; Search time 2513.83 Seconds
(without alignments)
10345.086 Million cell updates/sec

Title: US-09-737-297-2
Perfect score: 1070
Sequence: 1 gcccttgcacagatgcagc.....gtgttggaatgtaagggc 1070

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estda:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hnc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hnc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
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26: em_gss_pig:*
27: em_gss_vtl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	631	59.0	905	B2572385 msh2_2610
2	606.6	56.7	741	CD0422372 pshB040xf
3	591.4	55.3	28	BH771024 LMGtag74
4	581	54.3	9	AW600903 3B5 CDNA

5	571.8	53.4	650	10	BE636524
6	568.8	53.2	604	10	BE204135
7	566.4	52.9	641	14	CD040169
8	566.4	52.9	1033	29	B2561605
9	559	52.2	699	14	CD043647
10	557	52.1	559	10	BF845685
11	555.2	51.9	674	14	CD044496
12	548	51.2	1062	29	B2558387
13	540.6	50.5	1077	29	B2474941
14	539.8	50.4	1106	29	B2469058
15	531.6	49.7	995	28	BH700021
16	526	49.2	1106	29	B2569556
17	523.8	49.0	716	29	CNS01008
18	518.6	48.5	1078	29	B2569555
19	517	48.3	1082	29	B2459110
20	515.6	48.2	947	29	B246837
21	515.6	48.2	1020	29	BH688417
22	512	47.9	1079	28	BH705272
23	510.4	47.7	746	28	AQ957362
24	510.4	47.7	823	28	BH573967
25	508.2	47.5	862	28	BH527452
26	507.4	47.4	1010	29	B2431523
27	506.2	47.3	739	29	CNS01022
28	502	46.9	716	28	AQ957363
29	501.8	46.9	833	29	BH540327
30	501.4	46.9	1323	29	B2575698
31	501.2	46.8	889	29	B2462875
32	501.2	46.8	1016	29	B2426201
33	501	46.8	1053	29	B2447500
34	499.2	46.7	848	28	BH730827
35	498.2	46.6	810	29	B2490808
36	497.2	46.5	553	14	CD047311
37	497	46.4	834	29	B2449239
38	497	46.4	861	29	B2464776
39	495.4	46.3	812	28	BH594258
40	493.8	46.1	823	29	B2498828
41	492.8	46.1	569	9	A1779239
42	492	46.0	857	28	BH578853
43	491.8	46.0	845	28	BH564435
44	487	45.5	814	28	BH555249
45	484	45.2	850	28	BH677382

ALIGNMENTS

RESULT 1
B2572385
LOCUS
DEFINITION msh2_2610.y2 msh Pseudomonas aeruginosa genomic clone msh2_2610,
genomic survey sequence.
ACCESSION B2572385
VERSION B2572385.1 GI:27207446
KEYWORDS GSS.
SOURCE Pseudomonas aeruginosa
ORGANISM Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
REFERENCE 1 (bases 1 to 905)
Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M.,
Burns,J.L., Kaul,R. and Olsen,M.V.
TITLE Whole-Genome-Sequence Variation among Multiple Isolates of
Pseudomonas aeruginosa library
JOURNAL J. Bacteriol. (2002) In press
COMMENT Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun.
Location/Qualifiers

FEATURES

XX 29-NOV-2000; 2000MO-US42391.
 XX
 XX 29-NOV-1999; 99US-0168150.
 XX (AVIB-) AVI BIOPHARMA INC.
 XX
 XX Iversen Pl;
 XX WPI; 2001-45795/49.
 XX
 XX Antibacterial compound, useful for treating bacterial infections and as
 XX livestock and poultry food supplement, comprises antisense
 XX oligonucleotides complementary to bacterial 16S and 23S rRNA -
 XX
 XX Disclosure; Page - : 62pp; English.
 XX
 XX AAS11021-AAS11034 represent the coding sequences of bacterial 16S
 XX ribosomal RNA (rRNA) genes. The sequences were used to design anti-
 XX bacterial compounds comprising substantially unchanged antisense
 XX oligomers containing 8-40 nucleotide subunits, including a targeting
 XX nucleic acid sequence at least 10 nucleotides in length which is
 XX complementary to a bacterial 16S or 23S rRNA nucleic acid sequence.
 XX The antisense oligomers are used for treating a bacterial infection.
 XX In a human or a mammalian animal produced by *Escherichia coli*, *Salmonella*
 XX *typhimurium*, *Pseudomonas aeruginosa*, *Vibrio cholerae*, *Neisseria*
 XX *gonorrhoeae*, *Helicobacter pylori*, *Bartonella henselae*, *Haemophilus*
 XX *tuberculosis*, *Streptococcus pneumoniae*, *Treponema pallidum* and *Chlamydia*
 XX *trachomatis*. The antibacterial compound may be used as a food grain
 XX supplement in livestock and poultry food composition.
 XX Note: The present sequence is not shown in the specification but has
 XX been accessed from GenBank using the appropriate accession number given
 XX in the specification.
 XX
 XX Sequence 1467 BP; 370 A; 330 C; 458 G; 309 T; 0 other;

Query Match 84.8%; Score 907.4; DB 22; Length 1467;
 Best Local Similarity 93.9%; Pred. No. 1.2e-280;
 Matches 944; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 64 GCTTGCTTCTCTAGAGCGCGGAGGAGTAAAGCCTAGGAATCGCTGGTAGTG 123
 DB 10 GCTTGCTTCTCTAGATTCAGCGCGGAGGAGTAAAGCCTAGGAATCGCTGGTAGTG 69
 QY 124 GGGGATAACGTTCCGAAACGAGCGCTAATACCGCATACGTCCTACGGAGAAAGCAAGG 183
 DB 70 GGGGACAACGTTTGAAAGGACGCTAATACCGCATACGTCCTACGGAGAAAGCAAGG 129
 QY 184 ACCTTGGGCTTGGCGCTATCAGATGAGCCTAGTAGCTAGTGTGAGTAAAT 243
 DB 130 ACCTTGGGCTTGGCGCTATCAGATGAGCCTAGTAGCTAGTGTGAGTAAAT 189
 QY 244 GGCTCACCAGGCGAGCATCGTAACGTGTCTGAGAGGATGATCACTGGAAC 303
 DB 190 GGCTCACCAGGCGAGCATCGTAACGTGTCTGAGAGGATGATCACTGGAAC 249
 QY 304 AGAAGCGTCCAGCTCTTACGGAGGAGCAGCAGTGGGGAATATTGACAAATGGCGGAAG 363
 DB 250 AGAAGCGTCCAGCTCTTACGGAGGAGCAGCAGTGGGGAATATTGACAAATGGCGGAAG 309
 QY 364 CCTGATCCAGGCATGCGCGTGTGTGAAGAAGCTTTGGATTGAAAGCACTTAAGTT 423
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 QY 424 GGGAGGAAGGCTTGAATTAATCTGTGCAATTTTGAAGTTCAGCAGAAATTAAGCACC 483
 DB 370 GGGAGGAAGGCTTGAATTAATCTGTGCTTTTGAAGTTCAGCAGAAATTAAGCACC 429
 QY 484 GGCTAACTGTGTGCAGAGCGCGGTAATACAGAGGGTGCAGCGTTATCGGAATTAC 543
 DB 430 GGCTAACTGTGTGCAGAGCGCGGTAATACAGAGGGTGCAGCGTTATCGGAATTAC 489

QY 544 TGGGCGTAAAGCGCGGTAGTGTGTTTGAAGTTGATGTAATCCCGGGGCTCAACC 603
 DB 490 TGGGCGTAAAGCGCGGTAGTGTGTTTGAAGTTGATGTAATCCCGGGGCTCAACC 549
 QY 604 TGGGAATCATTTCAAACTGACTAGATAGTATGTAAGGAGTGTGTAATTTCTGT 663
 DB 550 TGGGAATCATTTCAAACTGACTAGATAGTATGTAAGGAGTGTGTAATTTCTGT 609
 QY 664 GTAGCGGTAAATGGGTAGATTAAGGAAGAAACCAAGTGGCGAAGCGACCACTGAC 723
 DB 610 GTAGCGGTAAATGGGTAGATTAAGGAAGAAACCAAGTGGCGAAGCGACCACTGAC 669
 QY 724 TAATCTGACACTGAGGTGCGAAAGCCTGGGAGCGAAACAGATTAATACCTGTAGT 783
 DB 670 TAATCTGACACTGAGGTGCGAAAGCCTGGGAGCGAAACAGATTAATACCTGTAGT 729
 QY 784 CCAAGCGGTAAACGATGCACTAGCCGTTGGAAGCCTTGAAGTGTGCGGACCTA 843
 DB 730 CCAAGCGGTAAACGATGCACTAGCCGTTGGAAGCCTTGAAGTGTGCGGACCTA 789
 QY 844 ACGATTAAGTGAACCGCTGGGAGTACGCGCCGCAAGGTTAAACTCAATGATTAAC 903
 DB 790 ACGATTAAGTGAACCGCTGGGAGTACGCGCCGCAAGGTTAAACTCAATGATTAAC 849
 QY 904 GGGGCGCGCAAGCGGTGAGCATGTGTTAATTGAAAGCAAGCGAAACCTTAC 963
 DB 850 GGGGCGCGCAAGCGGTGAGCATGTGTTAATTGAAAGCAAGCGAAACCTTAC 909
 QY 964 CAGGCTTGAATCAATGAAGAACTTCTAGATGATGATGAGGCTTGGGGAACATTGAGA 1023
 DB 910 CAGGCTTGAATCAATGAAGAACTTCTAGATGATGATGAGGCTTGGGGAACATTGAGA 969
 QY 1024 CAGGTGCTCATGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1068
 DB 970 CAGGTGCTCATGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1014

Search completed: January 30, 2004, 19:20:12
 Job time : 319.06 secs


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QY 1033 CATGCTGCTGACGCTGCTGTTGAAATGTAAG 1068
Db 1021 CATGCTGCTGACGCTGCTGTTGAAATGTTGGG 1056

RESULT 13
ID AAL50856
AL50856 standard; DNA; 1480 BP.
AC AAL50856;
AT 30-JAN-2003 (first entry)
DE Benzene-degrading bacteria-related DNA sequence #2.
KM Benzene-degrading bacteria; benzene decomposition; ds.
XX Unidentified.
OS
XX KR2002011552-A.
XX PN 08-FEB-2002.
XX PD 01-AUG-2000; 2000KR-0044629.
XX PF 01-AUG-2000; 2000KR-0044629.
XX PR 01-AUG-2000; 2000KR-0044629.
XX PA (SMSU) SAMSUNG EVERLAND INC.
XX PI Park UH;
XX DR WPI; 2002-572306/61.
XX PT Benzene-degrading bacteria and its utilization method -
XX PS Disclosure; Fig 1; 7P; Korean.
XX CC The invention comprises a strain of bacteria (Pseudomonas putida) that is
CC useful for decomposing high concentrations of benzene (higher than
CC 1500ppm). The present DNA sequence is shown in a figure of the
CC specification.
XX SQ Sequence 1480 BP; 376 A; 330 C; 463 G; 311 T; 0 other;

Query Match 90.9%; Score 972.8; DB 24; Length 1480;
Best Local Similarity 95.1%; Pred. No. 1.2e-301;
Matches 1004; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 13 ATTGAACGCTGCGGCAAGCCCTAACATGCAAGTCGCGGTAGAGAGAAGCTTGCTTC 72
Db 1 ATTGAACGCTGCGGCAAGCCCTAACATGCAAGTCGCGGTAGAGAGAAGCTTGCTTC 60
QY 73 TCTTGAGAGCGCGGCGAGCGGTGATGCTTGAATCTGCTGCTGCTGCTGCTGCTGCTG 132
Db 61 TCGATTGCGGCGGCGAGCGGTGATGCTTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
QY 133 GTTCGAAACGCGCTAATACGCGATAGCTCTTACGCGGAGAAAGAGGCGGACCTTCGCG 192
Db 121 GTTCGAAAGGAGCGCTAATACGCGATAGCTCTTACGCGGAGAAAGAGGCGGACCTTCGCG 180
QY 193 CTTGCGCTATCAATAGAGCTTGAAGTTCGATTGCTTGAATGTTGTTGTTGTTGTTGTTG 252
Db 181 CTTGCGCTATCAATAGAGCTTGAAGTTCGATTGCTTGAATGTTGTTGTTGTTGTTGTTG 240
QY 253 AGCGAGAGATCGTAACTGCTGCTGAGAGATGATCACTGGAACCTGAGACAGCT 312
Db 241 AGCGAGAGATCGTAACTGCTGCTGAGAGATGATCACTGGAACCTGAGACAGCT 300
QY 313 CCAAGCTCTTACGCGGAGGCAAGTGGGGATTTGGACAAATGGCGGAAAGCTTATCCA 372
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Db 301 CCAGACTCTTACGCGGAGGCGAGCGTGGGAAATTTGGAACAATGGCGGAAAGCTTATCCA 360
QY 373 GCCATGCGCGGTGTTGAAAGAAAGCTTCTGGAATTTGAAGCACTTTAAGTTGGAGAAAG 432
Db 361 GCCATGCGCGGTGTTGAAAGAAAGCTTCTGGAATTTGAAGCACTTTAAGTTGGAGAAAG 420
QY 433 GGTGTAGATTAACTCTGCAATTTTGAAGCTTACCGACAAATAGACACCGGCTAATCTC 492
Db 421 GGCAATTACCTTAATAGATTAGTGTGTTGACGTTACCGACAAATAGACACCGGCTAATCTC 480
QY 493 TGTGCGACGACCGCGGTAATACAGAGGTCGAAGGCTTAATCGGAATTAATCTGAGGCGTAA 552
Db 481 TGTGCGACGACCGCGGTAATACAGAGGTCGAAGGCTTAATCGGAATTAATCTGAGGCGTAA 540
QY 553 AGCGCGGTAGGTGTTTGTAAAGTTGATGTAATCCCGGCTCAACCTGCGAATCTG 612
Db 541 AGCGCGGTAGGTGTTTGTAAAGTTGATGTAATCCCGGCTCAACCTGCGAATCTG 600
QY 613 CATTCAAACTGACTGATAGATAGTATGATAGAGGCTGGAATTTCTGTTAGCGGTG 672
Db 601 CATTCAAACTGACTGATAGATAGTATGATAGAGGCTGGAATTTCTGTTAGCGGTG 660
QY 673 AATGCGTAGATATAGAGAGAAACACAGTGGCGAAGGCGACCACTGGAATATATCTGA 732
Db 661 AATGCGTAGATATAGAGAGAAACACAGTGGCGAAGGCGACCACTGGAATATATCTGA 720
QY 733 CACTGAGTGCAGAAAGCGTGGGAGAGCAACAGATTAATATCCTGTTAGTTCACGCCGT 792
Db 721 CACTGAGTGCAGAAAGCGTGGGAGAGCAACAGATTAATATCCTGTTAGTTCACGCCGT 780
QY 793 AAAGATGCTCACTTACCGCTTGAAGCCTTGAAGCTTTAGTGGCGACGTAACGATTA 852
Db 781 AAAGATGCTCACTTACCGCTTGAAGCCTTGAAGCTTTAGTGGCGACGTAACGATTA 840
QY 853 GTTGACCGCTGCGGAGTACGCGCCGAGGTTAAATCTCAATGATTAAGCGGGGCCCG 912
Db 841 GTTGACCGCTGCGGAGTACGCGCCGAGGTTAAATCTCAATGATTAAGCGGGGCCCG 900
QY 913 CACAAGCGGTGAGCATGATGTTTAATTGAGAGCAACGCGAAGAACTTACCAAGCCCTG 972
Db 901 CACAAGCGGTGAGCATGATGTTTAATTGAGAGCAACGCGAAGAACTTACCAAGCCCTG 960
QY 973 ACATCAATGAACTTTCTAGAGATGATGTCCTCGGGAACATTGAGACAGCTGCTG 1032
Db 961 ACATGACAGAACTTTCCAGAGATGATGTCCTCGGGAACCTGACACAGCTGCTG 1020
QY 1033 CATGCTGCTGACGCTGCTGTTGAAATGTTGGG 1068
Db 1021 CATGCTGCTGACGCTGCTGTTGAAATGTTGGG 1056

RESULT 14
ID AAT18764
AAT18764 standard; rRNA; 1518 BP.
AC AAT18764;
AT 05-JUL-1996 (first entry)
DE Pseudomonas aeruginosa 16S ribosomal RNA.
KM Atrazine; pesticide degradation; soil decontamination;
KM bioremediation; s-triazine; herbicide; se.
XX Pseudomonas aeruginosa.
OS
XX Key Location/Qualifiers
XX misc_difference 46
XX FT /tag= a
XX FT /note "base 46 is identified as 'n'"
XX FT misc_difference 221
XX FT /tag= b
```


CC compatible, functional polymers, such as device materials and soft
 CC medical materials. The present sequence represents the basic nucleotide
 CC sequence of 16S rRNA of *P. jessenii* strain Pl61, a microorganism isolated
 CC from soil that can produce PHAs.

XX
 SQ Sequence 1501 BP; 379 A; 339 C; 475 G; 308 T; 0 other;

Query Match 92.1%; Score 985.2; DB 24; Length 1501;

Best Local Similarity 95.9%; Pred. No. 1.3e-305; Mismatches 43; Indels 0; Gaps 0;

Matches 1011; Conservative 0;

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 DB 1 TGAAGCTGGGGGCGGCGCTTAACATGCGAGGTGAGAGAGAGCTTCTC 60
 QY 75 TTGAAGCGGGCGGAGCGGGTGAATGCTTAGAACTGCTGTAGTGGGGATTA 134
 DB 61 AATTGACGGCGGAGCGGGTGAATGCTTAGAACTGCTGTAGTGGGGATTA 120
 QY 135 TCGGAAACGGAGCGCTTAATCCGCATACCTCCAGGAGAAAGAGGCGGACCTTCGCGCC 194
 DB 121 CTCGAAAGGAGCGCTTAATCCGCATACCTCCAGGAGAAAGAGGAGACCTTCGCGCC 180
 QY 195 TTGCGCTATCAGATGAGCGCTAGGTGAGTGAATGCTAGTGTGAGGTAAAGCTCACCAG 254
 DB 181 TTGCGCTATCAGATGAGCGCTAGGTGAGTGAATGCTAGTGTGAGGTAAAGCTCACCAG 240
 QY 255 GCGACGATCCGTTAATCTGCTGAGAGATGATCACTGACATGAGACAGCGGTCC 314
 DB 241 GCGACGATCCGTTAATCTGCTGAGAGATGATCACTGACATGAGACAGCGGTCC 300
 QY 315 AGACTCTCAGGAGGAGCGAGCAGTGGGGAATATTGACATAGGCGAAAGCCTGATCCAGC 374
 DB 301 AGACTCTCAGGAGGAGCGAGCAGTGGGGAATATTGACATAGGCGAAAGCCTGATCCAGC 360
 QY 375 CATGCCGCTGTGTGAAGAAGGCTTCGGATTGAAGCACTTTAAGTTGGAGAGAGG 434
 DB 361 CATGCCGCTGTGTGAAGAAGGCTTCGGATTGAAGCACTTTAAGTTGGAGAGAGG 420
 QY 435 TTGTAGATTAATCTCTGCAATTTTGAAGTACCGAGAGAAACACCGGCTAATCTG 494
 DB 421 CATTAACCTTAATCTCTGCAATTTTGAAGTACCGAGAGAAACACCGGCTAATCTG 480
 QY 495 TGCAGACGCGCGGTAATACAGAGGGTCAAGCGTTAATCGGAATTAAGTGGGCGTAAG 554
 DB 481 TGCAGACGCGCGGTAATACAGAGGGTCAAGCGTTAATCGGAATTAAGTGGGCGTAAG 540
 QY 555 CGCGGTAGTGGTTTGTTAAGTGAATGTAATCCCGGGCTCAACCTGGAGACTGCA 614
 DB 541 CGCGGTAGTGGTTTGTTAAGTGAATGTAATCCCGGGCTCAACCTGGAGACTGCA 600
 QY 615 TTCAAAACTGACTGACTAGATGATGAGAGGGTGGTGAATTTCTGTGTAGCGGTAA 674
 DB 601 TTCAAAACTGACTGACTAGATGATGAGAGGGTGGTGAATTTCTGTGTAGCGGTAA 660
 QY 675 ATGCGTATGATATGAGAAAGAAACAGAGTGGGAAAGCGACCACTGAGCTAATCTACA 734
 DB 661 ATGCGTATGATATGAGAAAGAAACAGAGTGGGAAAGCGACCACTGAGCTAATCTACA 720
 QY 735 CTGAGGTGCGAAAGCGTGGGAGCAAAAGATTGATACCTGGTATGCCACCGCTAA 794
 DB 721 CTGAGGTGCGAAAGCGTGGGAGCAAAAGATTGATACCTGGTATGCCACCGCTAA 780
 QY 795 AGCATGTCACTAGCGCTTGAAGCGCTTGAAGCTTTAATGCGCAGCTTAAGCTTAAGT 854
 DB 781 AGCATGTCACTAGCGCTTGAAGCGCTTGAAGCTTTAATGCGCAGCTTAAGCTTAAGT 840
 QY 855 TGAACGCTGCGGAGTACGCGCGCAAGGTTAAACTCAATGAATGAACGCGGCGCGCA 914
 DB 841 TGAACGCTGCGGAGTACGCGCGCAAGGTTAAACTCAATGAATGAACGCGGCGCGCA 900
 QY 915 CAAGCGGTGAGAGATGTGTTTAATTCGAAGCAAGCAAGCACTTACAGGCTTGAC 974

DB 901 CAAGCGGTGAGAGATGTGTTTAATTCGAAGCAAGCAAGCACTTACAGGCTTGAC 960
 QY 975 ATCCATGATCTTTCTAGATGATGTTGCTCTCGGAAACATTGAGACAGTGTGCA 1034
 DB 961 ATCCATGATCTTTCTAGATGATGTTGCTCTCGGAAACATTGAGACAGTGTGCA 1020
 QY 1035 TGGCTGTGCTAGCTGCTGTGTTGAATGTAAAG 1068
 DB 1021 TGGCTGTGCTAGCTGCTGTGTTGAATGTAAAG 1054

RESULT 10

AA166302
 ID AA166302 standard; DNA; 1501 BP.

XX AA166302;

XX 22-JAN-2002 (first entry)

XX Pseudomonas jessenii coding sequence.

XX Polyhydroxyalkanoate; 3-hydroxythienylalkanoic acid; PHA;

XX medical material; biodegradable polymer; ds.

XX Pseudomonas jessenii.

PN EP130043-A2.

PD 05-SEP-2001.

XX 28-FEB-2001; 2001EP-0104922.

PR 29-FEB-2000; 2000JP-0054317.

PR 29-FEB-2000; 2000JP-0054667.

XX (CANO) CANON KK.

XX Horita T, Yano T, Kobayashi S, Imamura T, Kenmoku T, Kozaki S;

XX WPI; 2002-012494/02.

XX Novel polyhydroxy alkanates containing 3-hydroxy thienyl alkanolic acid

PT monomer units for use as biodegradable and functional polymers -

XX Disclosure; Page 32-33; 46p; English.

XX The present invention relates to polyhydroxy alkanates (PHA) containing

CC 3-hydroxy thienyl alkanolic acid monomer units. These can be used as

CC biodegradable, bio-compatible, functional polymers, as device material

CC and as soft medical material. The present sequence is a coding sequence

CC from Pseudomonas jessenii.

XX Sequence 1501 BP; 379 A; 339 C; 475 G; 308 T; 0 other;

SQ

Query Match 92.1%; Score 985.2; DB 24; Length 1501;

Best Local Similarity 95.9%; Pred. No. 1.3e-305; Indels 0; Gaps 0;

Matches 1011; Conservative 0; Mismatches 43;

QY 15 TGAAGCTGGGGGCGGCGCTTAACATGCGAGGTGAGAGAGAGCTTCTC 74

DB 1 TGAAGCTGGGGGCGGCGCTTAACATGCGAGGTGAGAGAGAGCTTCTC 60

QY 75 TTGAAGCGGGCGGAGCGGGTGAATGCTTAGAACTGCTGTAGTGGGGATTAAGT 134

DB 61 AATTGACGGCGGAGCGGGTGAATGCTTAGAACTGCTGTAGTGGGGATTAAGT 120

QY 135 TCGGAAACGGAGCGCTTAATCCGCATACCTCCAGGAGAAAGAGGCGGACCTTCGCGCC 194

DB 121 CTCGAAAGGAGCGCTTAATCCGCATACCTCCAGGAGAAAGAGGAGACCTTCGCGCC 180

QY 195 TTGCGCTATCAGATGAGCGCTAGGTGAGTGAATGCTAGTGTGAGGTAAAGCTCACCAG 254

DB 181 TTGCGCTATCAGATGAGCGCTAGGTGAGTGAATGCTAGTGTGAGGTAAAGCTCACCAG 240

PF	27-DEC-2000;	2000EP-0128540.	
XX			
PR	27-DEC-1999;	99JP-0371864.	
PR	27-DEC-1999;	99JP-0371867.	
PR	27-DEC-1999;	99JP-0371868.	
PR	27-DEC-1999;	99JP-0371869.	
PR	31-JAN-2000;	2000JP-0023024.	
PR	31-JAN-2000;	2000JP-0023025.	
PR	28-NOV-2000;	2000JP-0361323.	
XX			
PA	(CANO)	CANON KK.	
PI	Homma T, Kobayashi T, Yano T, Kobayashi S, Imamura T, Suda S;		
PI	Kemmoku T;		
XX			
DR	WPI; 2001-598513/68.		
PT	Polyhydroxyalkanoate comprises monomeric unit that has pendant		
PT	alkylaryl group, optionally substituted on benzene ring.		
PS			
XX	Disclosure; Fig 12; 95pp; English.		
CC	The present sequence represents that of the 16S rRNA (ribosomal RNA) gene		
CC	from <i>Pseudomonas jesseni</i> strain P161. Prior to the present invention,		
CC	strain P161 had not been assigned to a particular species; comparison		
CC	of the strain P161 16S rRNA gene DNA with 16S rRNA gene sequences of		
CC	known micro-organisms of the genus <i>Pseudomonas</i> identified P161 as a		
CC	strain of <i>Pseudomonas jesseni</i> . The specification describes a		
CC	polyhydroxyalkanoate comprising one or more monomeric units that have		
CC	pendant alkylaryl groups, optionally substituted on the benzene ring.		
CC	The specification also describes a process of producing the		
CC	polyhydroxyalkanoate by culturing a micro-organism in a medium containing		
CC	a raw material alkanoate and a yeast extract so that the alkanoate is		
CC	polymerised. The invention is used for the production of novel		
CC	polyalkanoates using microbial enzymes. The polymer is adhesive at		
CC	ambient temperatures and, when mixed with other polymers, reduces the		
CC	glass transition temperature of the blend. Orientation and crystallinity		
CC	can be tailored by changing the pendant substituent groups. The desired		
CC	polymer can be obtained without interference from unintended monomer		
XX	units.		
XX			
SQ	Sequence 1501 BP; 379 A; 339 C; 475 G; 308 T; 0 other;		
Query Match	92.1%; Score 985.2; DB 23; Length 1501;		
Best Local Similarity	95.9%; Pred. No. 1.3e-305;		
Matches 1011; Conservative	0; Mismatches 43; Indels 0; Gaps 0		
QY	15 TGAAGCCTGGCGGCGAGCCTTAACAATGCAAGTGGAGGCTAGAGAGAAAGCTTGCTTC	74	
DB	1 TGAAGCCTGGCGGCGAGCCTTAACAATGCAAGTGGAGGCTAGAGAGAAAGCTTGCTTC	60	
QY	75 TTGAGACGGCGGAGCGGCTGAATATGCTTGAAGATCTGCTGCTATGAGGGATATACGT	134	
DB	61 AATTCAGCGCGGAGCGGCTGAATATGCTTGAAGATCTGCTGCTATGAGGGATATACGT	120	
QY	135 TCGAAGACGAGCGCTATATCCGATACGCTCTTACCGGAGAAAGCAGGGAGACTTCGGGCC	194	
DB	121 CTGGAAGGAGCGCGCTATATCCGATACGCTCTTACCGGAGAAAGCAGGGAGACTTCGGGCC	180	
QY	195 TTGCGGTATCAGATGAGCGCTATGCTGAGATTGAGTATGTTGGTAGCTATATGGCTCACCAAG	254	
DB	181 TTGCGGTATCAGATGAGCGCTATGCTGAGATTGAGTATGTTGGTAGCTATATGGCTCACCAAG	240	
QY	255 GCGAGCATCCGTAATCTGATCTGAGAGATGATCAATGTCACACTGGAATCTGAGACAGGATCC	314	
DB	241 GCGAGCATCCGTAATCTGATCTGAGAGATGATCAATGTCACACTGGAATCTGAGACAGGATCC	300	
QY	315 AGACTCTCTACGGGAGGACAGTGGGGAATTTTGGACAAATGGGAGAAAGCTTATCCAGC	374	
DB	301 AGACTCTCTACGGGAGGACAGTGGGGAATTTTGGACAAATGGGAGAAAGCTTATCCAGC	360	
QY	375 CATGCCGCTGTGTGGAAGAGGTCTTCGAGATTGTAAGCACTTTAATTGGAGGAAGG	434	

Ds	361	CATGCCCGGTGTGAAAGAGGCTTTCGGATTGTAAAGCACTTAAAGTGGAGGAAAGG	420
Qy	435	TGTGAGATTATATCTCGCAATTTTGAAGTACCGACAGATTAGACCGGGTAACTGTG	494
Ds	421	CATTAACTAATAGCTTAGTGTGTTTGAACGTTACCGACAGATTAGACCGGGTAACTGTG	480
Qy	495	TGCCAGCAGCCGCGGTAAATACAGAGGGTGCAGCGTTAATCGGAATTACTGGGCGTAAAG	554
Ds	481	TGCCAGCAGCCGCGGTAAATACAGAGGGTGCAGCGTTAATCGGAATTACTGGGCGTAAAG	540
Qy	555	CCGGGTAGGTGTTTGTAGATTGGATGTGAATCCCCGGGCTCAACTGGGAACTGCA	614
Ds	541	CCGGGTAGGTGTTTGTAGATTGGATGTGAATCCCCGGGCTCAACTGGGAACTGCA	600
Qy	615	TTCAAAACTGACTGACTAGATATGTAGAGGGTGTGGAATTTCTGTGTAGCGGTGA	674
Ds	601	TTCAAAACTGACTGACTAGATATGTAGAGGGTGTGGAATTTCTGTGTAGCGGTGA	660
Qy	675	ATGCGTAGATATAGGAAGGAACACCAATGGCGGAAGGCGACCACTGGAATTACTGACA	734
Ds	661	ATGCGTAGATATAGGAAGGAACACCAATGGCGGAAGGCGACCACTGGAATTACTGACA	720
Qy	735	CTGAGGTGCGAAAGCGTGGGAGCGAAACAGAAATTAGTACCCTGTGTGTCCAGCCGTGA	794
Ds	721	CTGAGGTGCGAAAGCGTGGGAGCGAAACAGAAATTAGTACCCTGTGTGTCCAGCCGTGA	780
Qy	795	ACGATGTCAACTAGCCGCTGGGAACCTTTAGAGCGCAGCTAACGCACTTAAGT	854
Ds	781	ACGATGTCAACTAGCCGCTGGGAACCTTTAGAGCGCAGCTAACGCACTTAAGT	840
Qy	855	TGACCGCCTCGGGAGTACGCGCCGCAAGTTAAACTCCAAATGATTGACGCGCGCCGCA	914
Ds	841	TGACCGCCTCGGGAGTACGCGCCGCAAGTTAAACTCCAAATGATTGACGCGCGCCGCA	900
Qy	915	CAAGCGGTGAGGCAATGTGTTTATTGTGAAGCAAGCGGAACCTTACAGGCGCTGAC	974
Ds	901	CAAGCGGTGAGGCAATGTGTTTATTGTGAAGCAAGCGGAACCTTACAGGCGCTGAC	960
Qy	975	ATCCATGAACTTTCTAGAGATAGATTGTGCTTCGGGAACATTGAGACAGGTGCTGA	1034
Ds	961	ATCCATGAACTTTCTAGAGATAGATTGTGCTTCGGGAACATTGAGACAGGTGCTGA	1020
Qy	1035	TGGCTGTGCTCGAGCTCGTGTGTGAATGTGAAG	1068
Ds	1021	TGGCTGTGCTCGAGCTCGTGTGTGTGAATGTGTGG	1054
RESULT 8			
AAL39554			
ID	AAL39554 standard; DNA; 1501 BP.		
XX	AAL39554:		
AC			
DT	05-SEP-2002 (first entry)		
Ds	Pseudomonas jessenii Pl61 strain DNA.		
XX			
KM	Polyhydroxyalkanoate; PHA; benzoyl alkanolic acid; device material;		
XX	water repellent; medical material; Pseudomonas jessenii; Pl61 strain; ds.		
XX			
OS	Pseudomonas jessenii.		
FN	BP1188782-A2.		
PD	20-MAR-2002.		
PF	14-SEP-2001; 2001BP-0122101.		
PR	14-SEP-2000; 2000JP-0279900.		
PR	13-DEC-2000; 2000JP-0378827.		
PR	31-MAY-2001; 2001JP-0168238.		
PR	31-MAY-2001; 2001JP-0165509.		

XX 21-NOV-2001 (first entry)
 XX Pseudomonas jessenii 161 strain.
 XX Polyhydroxyalkanoate; alkanoate; microorganism; functional polymer; ds;
 XX medical material.
 XX Pseudomonas jessenii.
 XX EP1113033-A2.
 XX 04-JUL-2001.
 XX 22-DEC-2000; 2000EP-0128444.
 XX 27-DEC-1999; 99JP-0371863.
 XX 31-JAN-2000; 2000JP-0023078.
 XX 31-JAN-2000; 2000JP-0023080.
 XX 31-JAN-2000; 2000JP-0023083.
 XX 30-MAR-2000; 2000JP-0095011.
 XX 30-MAR-2000; 2000JP-0095013.
 XX 30-MAR-2000; 2000JP-0095013.
 XX 07-JUL-2000; 2000JP-0207089.
 XX 07-JUL-2000; 2000JP-0207091.
 XX 27-NOV-2000; 2000JP-0359789.
 XX (CANO) CANON KK.
 XX Honma T, Kobayashi T, Yano T, Kobayashi S, Imamura T, Suda S;
 XX Kennoku T;
 XX WPI; 2001-537748/60.
 XX New polyhydroxyalkanoates useful as functional polymers e.g. in medical
 XX devices -
 XX Claim 36; Page 83-84; 184pp; English.
 XX The invention relates to polyhydroxyalkanoates comprising monomer units
 XX of diverse structures containing side chain substituents. This sequence
 XX represents a Pseudomonas jessenii 161 strain microorganism, capable of
 XX synthesizing a polyhydroxyalkanoate from an alkanoate. By culturing a
 XX microorganism in a medium containing an alkanoate, a polyhydroxyalkanoate
 XX can be obtained. Polyhydroxyalkanoates are used as functional polymers,
 XX particularly in medical devices and materials. The use of microorganisms
 XX yields polymers of high purity and in high yield.
 XX Sequence 1501 BP; 379 A; 339 C; 475 G; 308 T; 0 other;
 SQ

Query Match 92.1%; Score 985.2; DB 22; Length 1501;
 Best Local Similarity 95.9%; Pred. No. 1.3e-305;
 Matches 1011; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 15 TGAACGCTGGCGGCGGCTTAACATGCAATGCAAGCGGTAGAGAGAACTTGTCTTC 74
 DB 1 TGAACGCTGGCGGCGGCTTAACATGCAATGCAAGCGGTAGAGAGAACTTGTCTTC 60
 QY 75 TTGAAGAGGCGGCGGCGGTAGTATGCTTAGAGAACTTGTCTGTAGTGGGGATTAACGT 134
 DB 61 AATTGAGGCGGCGGCGGTAGTATGCTTAGAGAACTTGTCTGTAGTGGGGATTAACGT 120
 QY 135 TCGAAGAGGCGGCGGTATACGCAATGCTCTTAGCGGAGAAAGAGGCGGCTTGGGGC 194
 DB 121 CTCGAAGAGGCGGCGGTATACGCAATGCTCTTAGCGGAGAAAGAGGCGGCTTGGGGC 180
 QY 135 TTGGGCTATCAGATGAGCGTGTGCGATTGCTAGTTGGTGAAGTATGGCTTCAACAAAG 254
 DB 181 TTGGGCTATCAGATGAGCGTGTGCGATTGCTAGTTGGTGAAGTATGGCTTCAACAAAG 240
 QY 255 GCGAGCATCGTAATGCTGTGAGAGATGATCGTACACTGGAATGAGACAGCGTCC 314
 DB 241 GCGAGCATCGTAATGCTGTGAGAGATGATCGTACACTGGAATGAGACAGCGTCC 300

QY 315 AGACTCTAGGAGGAGGAGGAGTGGGGAATATTGACATATGGGCGGAACCTGATCCAGC 374
 DB 301 AGACTCTAGGAGGAGGAGGAGTGGGGAATATTGACATATGGGCGGAACCTGATCCAGC 360
 QY 375 CATGCCCGGTGTGGAAGAGGTCTTCGATTGTAAAGCACTTAAAGTTGGAGAGAGG 434
 DB 361 CATGCCCGGTGTGGAAGAGGTCTTCGATTGTAAAGCACTTAAAGTTGGAGAGAGG 420
 QY 435 TTGATGATTAATCTCGCAATTTTGAAGTATCCAGAGAAATAGACCGGCTAATCTCG 494
 DB 421 CATTAACCTAATAGTATGATGTTTACGCTTACGACAGAAATAGACCGGCTAATCTCG 480
 QY 495 TGCCAGAGCGCGGATATACAGAGGAGTGAACCGTAAATTCGAAATTAATGAGCGTAAAG 554
 DB 481 TGCCAGAGCGCGGATATACAGAGGAGTGAACCGTAAATTCGAAATTAATGAGCGTAAAG 540
 QY 555 CGCGGATAGTGTGTTGTTAAAGTTGATGTAATATCCCGGAGCTCAACCTGAGAACTGCA 614
 DB 541 CGCGGATAGTGTGTTGTTAAAGTTGATGTAATATCCCGGAGCTCAACCTGAGAACTGCA 600
 QY 615 TTCAAACCTGACTGACTAGAGTATGTTAGAGGAGTGTGTAATTTCTGTGAGCGGTAA 674
 DB 601 TTCAAACCTGACTGACTAGAGTATGTTAGAGGAGTGTGTAATTTCTGTGAGCGGTAA 660
 QY 675 ATGCGTAGATATAGGAAGGAACACAGTGGCGGAGCGACCACTGGAATACTAGACA 734
 DB 661 ATGCGTAGATATAGGAAGGAACACAGTGGCGGAGCGACCACTGGAATACTAGACA 720
 QY 735 CTGAGGTGCGAAAGCGTGGGAGCAACAGATTAATACCTGTGATGCCAGCGGTAA 794
 DB 721 CTGAGGTGCGAAAGCGTGGGAGCAACAGATTAATACCTGTGATGCCAGCGGTAA 780
 QY 795 ACGATGTCACTAGCCGCTTGAAGCCTTAGCTTTAGTGGGCGCACTAACCATTAAGT 854
 DB 781 ACGATGTCACTAGCCGCTTGAAGCCTTAGCTTTAGTGGGCGCACTAACCATTAAGT 840
 QY 855 TGACCGCTTGGGAGATACGCGCGCAAGGTTAAATCTCAATGATTTGACGGGGCGCCGCA 914
 DB 841 TGACCGCTTGGGAGATACGCGCGCGCAAGGTTAAATCTCAATGATTTGACGGGGCGCCGCA 900
 QY 915 CAACGCGTGAAGCATGTGTTTAAATCGAAGCAACCGCAAGACCTTACAGGCGTTGAC 974
 DB 901 CAACGCGTGAAGCATGTGTTTAAATCGAAGCAACCGCAAGACCTTACAGGCGTTGAC 960
 QY 975 ATCCAAATGAACCTTTCTAGAGATAGATGTTGCTTCGGGAACTTGAACAGGTGCTGCA 1034
 DB 961 ATCCAAATGAACCTTTCTAGAGATAGATGTTGCTTCGGGAACTTGAACAGGTGCTGCA 1020
 QY 1035 TGCGTGTGCTACAGTGTGTTGGAATGTAAAG 1068
 DB 1021 TGCGTGTGCTACAGTGTGTTGGAATGTAAAG 1054

RESULT 7
 AA164177
 ID AA164177 standard; DNA; 1501 BP.
 XX AA164177;
 DT 26-FEB-2002 (first entry)
 XX Pseudomonas jessenii strain P161 16S rRNA gene sequence.
 XX 16S rRNA gene; strain P161; polyhydroxyalkanoate; alkydaryl group;
 XX alkanoate polymerization; microbial enzyme; glass transition temperature;
 XX adhesive; identification; ribosomal RNA; ds.
 XX Pseudomonas jessenii.
 XX EP1118629-A2.
 XX 25-JUL-2001.

QY 735 CTGAGGTGCGAAAGCTGGGGAGCAACAGATTAGATACCTGGTAGTCCACCCGTAA 794
|
|
|
Db 721 CTGAGGTGCGAAAGCTGGGGAGCAACAGATTAGATACCTGGTAGTCCACCCGTAA 780
|
|
|
QY 795 ACGATGTCAACTAGCGCTTGGAGAGCCTTTAGTGGCGCAGCTAACGCAATTAAGT 854
|
|
|
Db 781 ACGATGTCAACTAGCGCTTGGAGAGCCTTTAGTGGCGCAGCTAACGCAATTAAGT 840
|
|
|
QY 855 TGACCGCTGGGGAGTACGGCGCAAGGTTAAACTCAATGAATGAACGGGGGCGCGCA 914
|
|
|
Db 841 TGACCGCTGGGGAGTACGGCGCAAGGTTAAACTCAATGAATGAACGGGGGCGCGCA 900
|
|
|
QY 915 CAAGCGGTGAGCATGTGTTTAATTGAGCAACGCGAAGACCTTACAGGCTTGAC 974
|
|
|
Db 901 CAAGCGGTGAGCATGTGTTTAATTGAGCAACGCGAAGACCTTACAGGCTTGAC 960
|
|
|
QY 975 ATCCAAATGAACCTTTCTAGAGATAGATGTGCTGCTTGGGAACATTGAGACAGGTGCTGCA 1034
|
|
|
Db 961 ATCCAAATGAACCTTTCTAGAGATAGATGTGCTGCTTGGGAACATTGAGACAGGTGCTGCA 1020
|
|
|
QY 1035 TGCGTGTGTCAGCTGCTGTTGTAATGTAAG 1068
|
|
|
Db 1021 TGCGTGTGTCAGCTGCTGTTGTAATGTAAG 1054
|
|
|

RESULT 5

AAH77497 standard; DNA; 1501 BP.

AAH77497;

20-NOV-2001 (first entry)

Pseudomonas jessenii p161 coding sequence fragment.

Polyhydroxyalkanoate; PHA; ds.

Pseudomonas jessenii.

JP2001178485-A.

03-JUL-2001.

27-DEC-1999; 99JP-0371865.

27-DEC-1999; 99JP-0371865.

(CANO) CANON KK.

WPI; 2001-586288/66.

Production of a polyhydroxyalkanoate useful as a functional polymer -

Disclosure; Page 9; 12pp; Japanese.

The present invention describes a method of producing a polyhydroxyalkanoate (PHA) using a microbe. This may be Pseudomonas cichorii YN, Pseudomonas cichorii H45 or Pseudomonas jessenii p161. The PHA produced using the method of the invention is useful as a functional polymer. The present sequence is a fragment of the P. jessenii coding sequence.

Sequence 1501 BP; 379 A; 339 C; 475 G; 308 T; 0 other;

Query Match 92.1%; Score 985.2; DB 22; Length 1501;

Best Local Similarity 95.9%; Pred. No. 1.3e-305; Matches 1011; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 15 TGAACGCTGCGGAGCGCTTAACATGCAAGTCAGCGGTAGAGAGAGCTTGCTTC 74
|
|
|
Db 1 TGAACGCTGCGGAGCGCTTAACATGCAAGTCAGCGGTAGAGAGAGCTTGCTTC 60
|
|
|
QY 75 TTGAGAGCGGCGGAGCGGTGAGTATGCTTAGGAATTCGCTGATGAGGGGATTAACGT 134
|
|
|

Db 61 AATTGAGCGGCGGAGCGGTGAGTATGCTTAGGAATTCGCTGATGAGGGGCAACGTT 120
|
|
|
QY 135 TGGGAAAGGAGAGCTTAATACCGCATACGTTCTAGGGAGAAAGAGGGGACCTTGGGCC 134
|
|
|
Db 121 CTGGAAGGAGAGCTTAATACCGCATACGTTCTAGGGAGAAAGAGGGGACCTTGGGCC 180
|
|
|
QY 195 TTGCGCTATCAGATGAGCGCTAGTCCGATTAGTGTAGTGTAGATGATGCTACCAAG 254
|
|
|
Db 181 TTGCGCTATCAGATGAGCGCTAGTCCGATTAGTGTAGTGTAGATGATGCTACCAAG 240
|
|
|
QY 255 GCGAGATCCGTAATGCTGTGAGAGATGATCACTGCACTGGAATCTGAGACAGCGTCC 314
|
|
|
Db 241 GCGAGATCCGTAATGCTGTGAGAGATGATCACTGCACTGGAATCTGAGACAGCGTCC 300
|
|
|
QY 315 AGACTCTTACGGGAGGAGGAGCGGTGAGGAAATTGAGCAATGCGGCGAAAGCTGATCCAGC 374
|
|
|
Db 301 AGACTCTTACGGGAGGAGGAGCGGTGAGGAAATTGAGCAATGCGGCGAAAGCTGATCCAGC 360
|
|
|
QY 375 CATGCCGCGTGTGTAAGAGAGCTCTTGGAAATTGTAAGCACTTAACTTGGAGGAAAGG 434
|
|
|
Db 361 CATGCCGCGTGTGTAAGAGAGCTCTTGGAAATTGTAAGCACTTAACTTGGAGGAAAGG 420
|
|
|
QY 435 TTGTAGATTAATACCTGTCATTTTGAAGTGTGACGTACCGACAGAAATAGCACCGGCTAACCTG 434
|
|
|
Db 421 CATTAACCTTAATACCTGTCATTTTGAAGTGTGACGTACCGACAGAAATAGCACCGGCTAACCTG 480
|
|
|
QY 495 TGCCAGACAGCGCGGTATTAACAGAGGTGCAAGGCTTAATCGAATTAAGTGGCGTAAAG 554
|
|
|
Db 481 TGCCAGACAGCGCGGTATTAACAGAGGTGCAAGGCTTAATCGAATTAAGTGGCGTAAAG 540
|
|
|
QY 555 CCGCGGTAGGTGTTTGTAAAGTGTGATGTAAATTCGCCGGGCTCAACCTTGGGAACTGCA 614
|
|
|
Db 541 CCGCGGTAGGTGTTTGTAAAGTGTGATGTAAATTCGCCGGGCTCAACCTTGGGAACTGCA 600
|
|
|
QY 615 TTCAAACTGACTGACTAGATATGATGAGAGGTGAGGATTTCCGTGTAGCGGGTAA 674
|
|
|
Db 601 TTCAAACTGACTGACTAGATATGATGAGAGGTGAGGATTTCCGTGTAGCGGGTAA 660
|
|
|
QY 675 ATGCGTATATAGGAGAGAAACACCAAGTGGGAAAGCGGACCACTGACTAATATGACA 734
|
|
|
Db 661 ATGCGTATATAGGAGAGAAACACCAAGTGGGAAAGCGGACCACTGACTAATATGACA 720
|
|
|
QY 735 CTGAGGTGGAAGAGCGTGGGAGCAACAGATTAAGTATCCGTGTGTCACAGCGCTAA 794
|
|
|
Db 721 CTGAGGTGGAAGAGCGTGGGAGCAACAGATTAAGTATCCGTGTGTCACAGCGCTAA 780
|
|
|
QY 795 ACGATGTCAACTAGCGCTTGGAGAGCCTTTAGTGGCGCAGCTAACGCAATTAAGT 854
|
|
|
Db 781 ACGATGTCAACTAGCGCTTGGAGAGCCTTTAGTGGCGCAGCTAACGCAATTAAGT 840
|
|
|
QY 855 TGACCGCTGGGGAGTACGGCGCAAGGTTAAACTCAATGAATTAAGCGGGGCGCGCA 914
|
|
|
Db 841 TGACCGCTGGGGAGTACGGCGCAAGGTTAAACTCAATGAATTAAGCGGGGCGCGCA 900
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|
|
QY 915 CAAGCGGTGAGCATGTGTTTAATTGCAAGCAACGCGAAGACCTTACAGGCTTGAC 974
|
|
|
Db 901 CAAGCGGTGAGCATGTGTTTAATTGCAAGCAACGCGAAGACCTTACAGGCTTGAC 960
|
|
|
QY 975 ATCCAAATGAACCTTTCTAGAGATAGATGTGCTGCTTGGGAACATTGAGACAGGTGCTGCA 1034
|
|
|
Db 961 ATCCAAATGAACCTTTCTAGAGATAGATGTGCTGCTTGGGAACATTGAGACAGGTGCTGCA 1020
|
|
|
QY 1035 TGCGTGTGTCAGCTGCTGTTGTAATGTAAG 1068
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|
|
Db 1021 TGCGTGTGTCAGCTGCTGTTGTAATGTAAG 1054
|
|
|

RESULT 6

AAH12097 standard; DNA; 1501 BP.

AAH12097;

Db 241 GCGACGATCCGTAAGTCTGAGGAGTATGATCACTGAACTGAGACACGGCTCC 300
 QY 315 AGACTCTACGGGAGGAGCAGCAGTGGGGAATATTGAGACATGGCGGAAGCCTGATCCAG 374
 Db 301 AGACTCTACGGGAGGAGCAGCAGTGGGGAATATTGAGACATGGCGGAAGCCTGATCCAG 360
 QY 375 CATGCCGCTGTGTGTAAGAAGGTCTTCGGATTTGTAAGCACTTTAACTTTGGGAGGAAGG 434
 Db 361 CATGCCGCTGTGTGTAAGAAGGTCTTCGGATTTGTAAGCACTTTAACTTTGGGAGGAAGG 420
 QY 435 TTGTAGATTAACTCTGCAATTTTGAAGTTCGAGACGAGATAGCAACCGGCTAATCTG 494
 Db 421 CATTAACCTAATAGCTTAGTGTGTTGAGCTTACCGAGAGATAGCAACCGGCTAATCTG 480
 QY 495 TCCCGACAGCCCGGTAATACAGAGGTGCAAGCTTATGCAATTAATCTGCGGCTAAAG 554
 Db 481 TCCCGACAGCCCGGTAATACAGAGGTGCAAGCTTATGCAATTAATCTGCGGCTAAAG 540
 QY 555 CCGCGGTAGTGTGTTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAG 614
 Db 541 CCGCGGTAGTGTGTTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAG 600
 QY 615 TTCAAACTGACTGACTAGTATGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAG 674
 Db 601 TTCAAACTGACTGACTAGTATGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAG 660
 QY 675 ATGGGTAGTATAGGAAGGAACACAGTGGCGAAGGAGGACCACTGGAATTAATAGTACA 734
 Db 661 ATGGGTAGTATAGGAAGGAACACAGTGGCGAAGGAGGACCACTGGAATTAATAGTACA 720
 QY 735 CTGAGGTGCGAAAGCGTGGGAGCAACAGGATTAATGATACCTGCTGATGCAAGCGGTA 794
 Db 721 CTGAGGTGCGAAAGCGTGGGAGCAACAGGATTAATGATACCTGCTGATGCAAGCGGTA 780
 QY 795 ACGATGCACTAGCCCTGTTGGAACCTTTGAGCTTTTGTGGCGGAGTAACTGATTAAGT 854
 Db 781 ACGATGCACTAGCCCTGTTGGAACCTTTGAGCTTTTGTGGCGGAGTAACTGATTAAGT 840
 QY 855 TGACCGCTGCGGAGTACGCGCGGCAAGGTTAACTGAAATGATTAATGATTAATGATTAATG 914
 Db 841 TGACCGCTGCGGAGTACGCGCGGCAAGGTTAACTGAAATGATTAATGATTAATGATTAATG 900
 QY 915 CAAAGGCTGAGCATGTGTGTTAATTGGAAGCAACGCGGAACCTTACCAAGCCTTGAAC 974
 Db 901 CAAAGGCTGAGCATGTGTGTTAATTGGAAGCAACGCGGAACCTTACCAAGCCTTGAAC 960
 QY 975 ATCCATGAACTTTCTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1034
 Db 961 ATCCATGAACTTTCTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
 QY 1035 TGGCTGTGCTAGCTGCTGTTGTGAAATGTAAG 1068
 Db 1021 TGGCTGTGCTAGCTGCTGTTGTGAAATGTAAG 1054
 RESULT 4
 AAI64998
 ID AAI64998 standard; DNA; 1501 BP.
 AC AAI64998;
 XX 11-DEC-2001 (first entry)
 XX
 DE Polyhydroxyalkanoic acid related Pseudomonas jessenii coding sequence.
 XX
 XX Polyhydroxyalkanoic acid; PHA; biodegradable plastic; ds.
 XX OS Pseudomonas jessenii.
 XX JP2001178464-A.
 XX
 PD 03-JUL-2001.

XX 27-DEC-1999; 99JP-0371866.
 PF
 XX 27-DEC-1999; 99JP-0371866.
 PR
 XX
 XX (CANO) CANON KK.
 PA
 XX
 DR WPT: 2001-592589/67.
 XX
 XX
 PT Microbial preparation of polyhydroxyalkanoic acids, using new carbon
 PT sources useful as raw material for biodegradable plastics -
 PS
 XX
 XX Disclosure; Page 9; 10pp; Japanese.
 CC The present invention relates to the production of
 CC polyhydroxyalkanoic acids. These can then be used in the production of
 CC biodegradable plastics. The present sequence is a Pseudomonas jessenii
 CC coding sequence described in the exemplification of the invention.
 XX
 SQ Sequence 1501 BP; 379 A; 339 C; 475 G; 308 T; 0 other;

Query Match 92.1%; Score 985.2; DB 22; Length 1501;
 Best Local Similarity 95.9%; Pred. No. 1,3e-305;
 Matches 1011; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 15 TGAACGCTGCGGAGGCTTAACATGACAGTGCAGCGGTAGAGGAAGCTTGCTCTC 74
 Db 1 TGAACGCTGCGGAGGCTTAACATGACAGTGCAGCGGTAGAGGAAGCTTGCTCTC 60
 QY 75 TTGAGAGCGCGGAGGCTGATGATGCTTACAGATCTGCTGTAGTGGGAGTAACTG 134
 Db 61 AATTACACCGCGGAGGCTGATGATGCTTACAGATCTGCTGTAGTGGGAGTAACTG 120
 QY 135 TCGGAACGGAAGCGCTAATACCGATACGCTTACGGAAGGAAGCAAGGAGCCTTGCGGCC 194
 Db 121 CTGGAAGGGAAGCGCTAATACCGATACGCTTACGGAAGGAAGCAAGGAGCCTTGCGGCC 180
 QY 195 TTGCGCTATGATGAGCCCTAGTGCAGTATGATGATGATGATGATGATGATGATGATGATG 254
 Db 181 TTGCGCTATGATGAGCCCTAGTGCAGTATGATGATGATGATGATGATGATGATGATGATG 240
 QY 255 GCGACGATCCGCTAATGCTGTGAGAGATGATGATGATGATGATGATGATGATGATGATG 314
 Db 241 GCGACGATCCGCTAATGCTGTGAGAGATGATGATGATGATGATGATGATGATGATGATG 300
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 Db 301 AGACTCTACGGGAGGAGCAGCAGTGGGGAATATTGAGACATGGCGGAAGCCTGATCCAGC 360
 QY 375 CATGCCGCTGTGTGTAAGAAGGTCTTCGGATTTGTAAGCACTTTAACTTTGGGAGGAAGG 434
 Db 361 CATGCCGCTGTGTGTAAGAAGGTCTTCGGATTTGTAAGCACTTTAACTTTGGGAGGAAGG 420
 QY 435 TTGTAGATTAACTCTGCAATTTTGAAGTTCGAGACGAGATAGCAACCGGCTAATCTG 494
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 Db 481 TCCCGACAGCCCGGTAATACAGAGGTGCAAGCTTATGCAATTAATCTGCGGCTAAAG 540
 QY 555 CCGCGGTAGTGTGTTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAG 614
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 QY 675 ATGGGTAGTATAGGAAGGAACACAGTGGCGAAGGAGGACCACTGGAATTAATAGTACA 734
 Db 661 ATGGGTAGTATAGGAAGGAACACAGTGGCGAAGGAGGACCACTGGAATTAATAGTACA 720

PT Preparing anti-freeze peptides useful in frozen food products, e.g.
PT frozen vegetables and confectionery, by culturing bacteria from aqueous
PT low-temperature environment and extracting anti-freeze proteins from
PT culture

Claim 3, Page 56, 59pp; English.

CC The present sequence represents the 16S rRNA of *Pseudomonas* sp.,
CC isolate 20. Anti-freeze proteins can be isolated from *Pseudomonas* sp.,
CC using the method of the invention. The specification describes a method
CC for producing anti-freeze peptides (AFPs). The method comprises
CC collecting one or more samples of bacteria from an aqueous
CC low-temperature environment, culturing the bacteria and extracting
CC proteins from the samples, testing the proteins for anti-freeze
CC properties, selecting proteins having anti-freeze properties and
CC producing the selected protein for use as an AFP food additive. The
CC method is useful for producing AFPs which are incorporated in food
CC products, such as frozen vegetables and frozen confectionery such as
CC ice-cream. AFPs are useful in frozen food products, such as vegetables,
CC sauces, soups, snacks, dairy products and frozen confectionery, which
CC includes sorbet, water-ice, granites, frozen fruit purees and
CC milk-containing frozen products such as ice-cream, frozen yogurt or
CC custards, sherbet and ice-milk.

XX Sequence 1070 BP, 280 A, 223 C, 336 G, 231 T, 0 other;

SQ Query Match 100.0%; Score 1070; DB 22; Length 1070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCCTTGCTGATGAAACGCTGGCGGACGCTTAACACATGCAAGTCAGCGGTAGAGA 60
DB 1 GCCCTTGCTGATGAAACGCTGGCGGACGCTTAACACATGCAAGTCAGCGGTAGAGA 60
QY 61 GAAGCTTGCTCTCTTGAAGAGCGGCGAGCGGTAGATGCTAGAAATCTGCTGCTGATA 120
DB 61 GAAGCTTGCTCTCTTGAAGAGCGGCGAGCGGTAGATGCTAGAAATCTGCTGCTGATA 120
QY 121 GTGGGGGATTAAGTTCGAAAACGAGCGCTTAATACCGCATACGCTCTCAACGAGAAAGCAG 180
DB 121 GTGGGGGATTAAGTTCGAAAACGAGCGCTTAATACCGCATACGCTCTCAACGAGAAAGCAG 180
QY 181 GGAGCTTGCTGGCGCTTGGCGATGATGAGCGCTAGAGTTCGATGCTGCTGCTGCTGCTGCT 240
DB 181 GGAGCTTGCTGGCGCTTGGCGATGATGAGCGCTAGAGTTCGATGCTGCTGCTGCTGCTGCT 240
QY 241 AATGCTTCCACCAAGGCGACGATCCGTAATGCTGTAAGAGATGATCACTGGA 300
DB 241 AATGCTTCCACCAAGGCGACGATCCGTAATGCTGTAAGAGATGATCACTGGA 300
QY 301 CTGAGACACGCGTCCAGCTCTGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
DB 301 CTGAGACACGCGTCCAGCTCTGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
QY 361 AAGCTGATCCAGCCATGCGCGGTGTGTAAGAGGCTTCGCGATTGTAAGCACTTAA 420
DB 361 AAGCTGATCCAGCCATGCGCGGTGTGTAAGAGGCTTCGCGATTGTAAGCACTTAA 420
QY 421 GTTGGGAGGAAGGCTTGTAGATTAACTCTGCAATTTTGAAGCTTCCAGAGATAGAC 480
DB 421 GTTGGGAGGAAGGCTTGTAGATTAACTCTGCAATTTTGAAGCTTCCAGAGATAGAC 480
QY 481 ACCGGCTAACTCTGTGCAGAGCGCGGTATATACAGAGGCTCAAGCTTATCGGAAT 540
DB 481 ACCGGCTAACTCTGTGCAGAGCGCGGTATATACAGAGGCTCAAGCTTATCGGAAT 540
QY 541 TACTGGGCGTAAACCGCGGTAGGTGTTGTTAAGTTGATGTAATCCCGGCGCTCA 600
DB 541 TACTGGGCGTAAACCGCGGTAGGTGTTGTTAAGTTGATGTAATCCCGGCGCTCA 600
QY 601 ACCTGGGAACCTGATCAAAATGACTGATAGATGATGATGATGATGATGATGATGATGAT 660
DB 601 ACCTGGGAACCTGATCAAAATGACTGATAGATGATGATGATGATGATGATGATGATGAT 660

QY 661 TGTGTAGCGGTGAATGCGTATATATAGAGAAACACCAATGCGGAAAGCGCACCTG 720
DB 661 TGTGTAGCGGTGAATGCGTATATATAGAGAAACACCAATGCGGAAAGCGCACCTG 720
QY 721 GACTTAATCTGACACTGAGGTGGGAAAGCGTGGGAGCAACAGGATAGATTAACCTG 780
DB 721 GACTTAATCTGACACTGAGGTGGGAAAGCGTGGGAGCAACAGGATAGATTAACCTG 780
QY 781 AGTCACGCGGTAAACGATGTCACTAGCCGTTGGAAGCTTGAAGCTTGAAGCGGAG 840
DB 781 AGTCACGCGGTAAACGATGTCACTAGCCGTTGGAAGCTTGAAGCTTGAAGCGGAG 840
QY 841 CTAAAGCATTAATTAACCGCTGGGAGGATAGGCGCAAGGTTAAATCTAAATGAT 900
DB 841 CTAAAGCATTAATTAACCGCTGGGAGGATAGGCGCAAGGTTAAATCTAAATGAT 900
QY 901 GACGGGGGCGCGGACAAAGCGGTGAGCATGTGTTAAATTCGAAGCAACGGAAGACCT 960
DB 901 GACGGGGGCGCGGACAAAGCGGTGAGCATGTGTTAAATTCGAAGCAACGGAAGACCT 960
QY 961 TACCAAGCCTTGACATCCCAATGAATCTTCTAGAGATAGATGCTGCTTGGGAAACAT 1020
DB 961 TACCAAGCCTTGACATCCCAATGAATCTTCTAGAGATAGATGCTGCTTGGGAAACAT 1020
QY 1021 AGACAGGTGCTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1070
DB 1021 AGACAGGTGCTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1070

RESULT 2
AB076131
ID AB076131 standard; DNA, 1424 BP.

XX AB076131;

XX 13-JAN-2003 (first entry)

DE Rhodococcus AM12 16S rRNA DNA.

XX Plasmid stability protein; replication protein; ethylene forming enzyme;
XX carotenoid biosynthesis enzyme; isoprenoid; pyruvate decarboxylase;
XX polyhydroxyalkanoic acid synthase; PHA synthase; nitrile hydratase;
XX alcohol dehydrogenase; terpene synthase; cholesterol oxidase;
XX shuttle vector; 16S rRNA; ds.

OS Rhodococcus erythropolis.

XX W020025709-A2.

XX 18-JUL-2002.

XX 12-DEC-2001; 2001WO-US47868.

XX 12-DEC-2000; 2000US-254868P.

XX (DUPO) DU PONT DE NEMOURS & CO E. I.

XX Bramucci MG, Cheng Q, Kostichka KN, Tomb J;

XX WPI; 2002-557827/59.

XX New nucleic acid molecule encoding replication protein/plasmid
XX stability protein, useful in cloning and expression vectors,
XX particularly shuttle vectors for expression of heterologous genes in
XX Rhodococcus species

XX Example 1; Page 83-84; 96pp; English.

CC This invention describes a novel nucleic acid encoding a replication
CC protein or a plasmid stability protein. The product of the invention is
CC useful for expression of nucleic acid such as genes encoding enzymes
CC involved in the production of isoprenoid molecules, polyhydroxyalkanoic

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OM nucleic - nucleic search, using sw model

Run on: January 30, 2004, 08:32:25 ; Search time 316.06 Seconds
(without alignments)
9138.760 Million cell updates/sec

Title: US-09-737-297-2

Perfect score: 1070

Sequence: 1 gcccttgctcagattgaacg.....gtctgtgtaagttaagggc 1070

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0 %
Maximum Match 100 %

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1070	100.0	1070	22	AAH25692
2	990	92.5	1424	22	ABQ76131
3	985.2	92.1	1501	22	AA164997
4	985.2	92.1	1501	22	AA164998
5	985.2	92.1	1501	22	AAH77497
6	985.2	92.1	1501	22	AAH2097
7	985.2	92.1	1501	23	AA164177
8	985.2	92.1	1501	24	AA139554

9	985.2	92.1	1501	24	AA167771	Nucleotide sequenc
10	985.2	92.1	1501	22	AA166302	Pseudomonas jessen
11	982.8	91.9	1281	22	AA190025	Nucleotide sequenc
12	976	91.2	1480	24	AA150855	Benzene-degrading
13	972.8	90.9	1480	24	AA150856	Benzene-degrading
14	918.8	85.9	1518	17	AA118764	Pseudomonas aerugi
15	907.4	84.8	1467	22	AA111023	Pseudomonas aerugi
16	872.4	81.5	1535	20	AA183571	16S rRNA gene frag
17	856	80.0	1537	19	AA124291	Pseudomonas aerugi
18	830.6	77.6	1485	22	AA125691	Nucleotide sequenc
19	821.4	76.8	1528	20	AA183570	16S rRNA gene frag
20	818.2	76.5	1535	20	AA183568	16S rRNA gene frag
21	815	76.2	1529	20	AA183567	16S rRNA gene frag
22	815	76.2	1535	20	AA183569	16S rRNA gene frag
23	813.4	76.0	1529	20	AA183565	16S rRNA gene frag
24	813.4	76.0	1529	20	AA183566	16S rRNA gene frag
25	808.6	75.6	1529	20	AA183564	16S rRNA gene frag
26	808	75.5	15105	20	AA124989	E. coli MG1655 rrm
27	807	75.4	1494	25	ABX16312	Aliphatic hydrocar
28	806.6	75.4	1489	24	ABX16312	Klebsiella pneumon
29	801	74.9	1487	22	AA11034	Shigella dysenteria
30	798.4	74.6	1542	17	AA129140	rRNA gene (rrs) f
31	798.4	74.6	1542	22	AA175410	E. coli 16S rRNA..
32	798.4	74.6	1542	22	AA175410	Escherichia coli r
33	798.4	74.6	1542	24	ABN85800	Escherichia coli 1
34	798.4	74.6	15097	20	AA124983	E. coli MG1655 rrm
35	798.4	74.6	15098	20	AA124984	E. coli MG1655 rrm
36	798.2	74.6	1540	20	AA191514	Escherichia coli 1
37	797.8	74.6	1506	24	ABX16313	Escherichia coli 1
38	797.2	74.5	1541	20	AA124986	E. coli MG1655 rrm
39	796.8	74.5	1542	22	AA123015	E. coli 16S rRNA s
40	795.2	74.3	1461	24	ABX16312	Yersinia pestis 16
41	793.6	74.2	15014	20	AA124987	E. coli MG1655 rrm
42	793.4	74.1	1473	17	AA118760	Atrazine-degrading
43	792	74.0	1528	22	AA176235	Cycloclasticus pug
44	792	74.0	1542	14	AA164119	E. coli 16S rRNA f
45	792	74.0	1566	17	AA118645	16S ribosomal RNA

ALIGNMENTS

RESULT 1	AAH25692	AAH25692 standard; DNA; 1070 BP.
ID	AAH25692	
AC	AAH25692;	
XX		
DT	05-SEP-2001 (first entry)	
XX		
DE	Nucleotide sequence of 16S rRNA of Pseudomonas sp.	
XX		
KW	16S rRNA; anti-freeze protein; food additive; frozen vegetable;	
KW	frozen confectionery; ss.	
XX		
OS	Pseudomonas sp.	
XX		
PN	WO200144275-A2.	
XX		
PD	21-JUN-2001.	
XX		
PF	05-DEC-2000; 2000MO-EP12396.	
XX		
PR	15-DEC-1999; 99GB-0023696.	
XX		
PA	(UNITL) UNILEVER PLC.	
PA	(UNITL) UNILEVER NV.	
PA	(HIND-) HINDUSTAN LEVER LTD.	
XX		
PI	Berry M., Griffiths A., Hill P., Laybourne-Parry J., Mills S.,	
XX		
DR	WPI; 2001-398120/42.	
XX		


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Db      601 GGGAACTGCATTGAAAACCTGACTAGAGTATGTTAGAGGGGTGTGAATTTCCTGTG 660
QY      665 TAGCGGTGAATTCGTAGATATAGAGAGAACCAAGTGGCGAAGCCACCACTGTGACT 724
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QY      785 CAGCGCGTAAACGATGTCAACTAGCCGTTGGAAGCCTTGAGCTTTAGTGGCGAGCTAA 844
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QY      845 CGCATTAAGTTGACCGCTGGGGAGTACGGCCGCAAGTTAAACTCAAAATGAATTGACG 904
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QY      965 AGGCTTGACATCCAAATGAACCTTCTAGAGATAGATTGTGCTTCGGAACATTGAGAC 1024
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QY      1025 AGGTGCTGCATGCTGCTGCTGAGCTGCTGTTGTTGTAATGTAAAG 1068
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Search completed: January 30, 2004, 22:02:57
 Job time : 4088.5 secs

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 Db 724 CTAACTGCACTGAGGTGCGAAAGCGTGGGAGCAACAGATTTAGATCCCTGGTAG 783
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 Db 784 TCCACGCGGTAAAGCATGTCAATAGCCGTTGAAAGCTTGAAGCTTTAGTGGAGCT 843
 QY 843 AACGATTAAGTTGACCGCTGGGAGATAGCGCGCAAGTTAAATCTCAATGAATTGA 902
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 Db 1024 ACAGGTGCTGATGCTGTCTCAAGCTTCGTTTGTGAATGAAG 1069

RESULT 15
 AF451270 1483 bp DNA linear BCT 25-NOV-2002
 LOCUS Pseudomonas sp. E102 16S ribosomal RNA gene, partial sequence.
 DEFINITION AF451270.1 GI:18092524
 ACCESSION AF451270.1
 VERSION
 KEYWORDS
 SOURCE Pseudomonas sp. E102
 ORGANISM Pseudomonas sp. E102
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 Pseudomonadaceae; Pseudomonas.
 REFERENCE 1 (bases 1 to 1483)

AUTHORS Spanggaard, B., Huber, I., Nielsen, J., Sick, E. B., Pipper, C. B.,
 TITLE Martinussen, T., Slierendrecht, W. J., and Gram, L.
 JOURNAL The probiotic potential against vibriosis of the indigenous
 MEDLINE microflora of rainbow trout
 PUBMED Environ. Microbiol. 3 (12), 755-765 (2001)
 21835725
 11846769
 2 (bases 1 to 1483)
 REFERENCES Spanggaard, B., Huber, I., Nielsen, J., Sick, E. B., Pipper, C. B.,
 Martinussen, T., Slierendrecht, W. J., and Gram, L.
 TITLE Direct Submission
 JOURNAL Submitted (22-NOV-2001) Department of Seafood Research, c/o
 Technical University of Denmark, Danish Institute for Fisheries
 Research, Soltofte Plads, Kongens Lyngby, Copenhagen DK-2800,
 Denmark
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REFERENCE 2 (bases 1 to 1470)
 AUTHORS Godfrey,S.A.C., Harrow,S.A., Marshall,J.W. and Klena,J.D.
 TITLE Direct Submission
 JOURNAL Submitted (28-NOV-2000) Integrated Crop Protection, Crop & Food Research Ltd., Private Bag 4704, Christchurch 8152, New Zealand

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 VERSION AF057645.1 GI:3047379
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 ORGANISM Pseudomonas libanensis
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REFERENCE 1 (bases 1 to 1516)
 Daboussi,F., Hamze,M., Elomari,M., Verhille,S., Baida,N., Izard,D. and Leclerc,H.
 Pseudomonas libanensis sp. nov., a new species isolated from Lebanese spring waters
 Int. J. Syst. Bacteriol. 49 Pt 3, 1091-1101 (1999)

JOURNAL MEDLINE 99354498
 PUBMED 10425766
 2 (bases 1 to 1516)

REFERENCE Daboussi,F., Hamze,M., Verhille,S., Baida,N., Izard,D. and Leclerc,H.
 Direct Submission
 Submitted (07-Apr-1998) Bacteriological Laboratory, Medical University, 1 place de Verdun, Lille 59045, France

TITLE JOURNAL
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 REFERENCE 1 (bases 1 to 1500)
 AUTHORS Pirttila,A.M., Laukkanen,H., Pospiech,H., Wyllyla,R. and Hohnola,A.
 TITLE Detection of intracellular bacteria in the buds of Scotch pine (*Pinus sylvestris* L.) by in situ hybridization
 JOURNAL Appl. Environ. Microbiol. 66 (7), 3073-3077 (2000)
 MEDLINE 20336462
 PUBMED 10877808
 REFERENCE 2 (bases 1 to 1500)
 AUTHORS Pirttila,A.M., Laukkanen,H., Pospiech,H., Wyllyla,R. and Hohnola,A.

TITLE Direct Submission
 JOURNAL Submitted (15-MAY-2000) Department of Biology/Botany, University of
 Culu, POB 3000, Culu FIN-90014, Finland
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the Fluorescent Pseudomonads
 Unpublished
 2 (bases 1 to 1355)
 Gaidick, M., Plasmeyer, M.L., Blaine, L.D., Pienta, P.A. and
 Gillevet, P.M.
 TITLE
 Direct Submission
 Submitted (25-SEP-1998) Microbial Authentication Resource, American
 Type Culture Collection, 10801 University Blvd, Manassas, VA
 20110-2209, USA

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 ORGANISM
 Pseudomonas synxantha
 Pseudomonas synxantha
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 REFERENCE
 1 Berry, M.J., Griffiths, A.U., Hill, P.J., Laybourne-Parry, J. and
 Mills, S.V.
 Processes and organisms for the production of anti-freeze proteins
 Patent: WO 0144275-A 5 21-JUN-2001;
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ACCESSION AY014824
VERSION AY014824.1 GI:17220742
KEYWORDS
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.

REFERENCE
1 (bases 1 to 1461)
Godfrey, S.A.C., Harrow, S.A., Marshall, J.W. and Klena, J.D.
Characterization of *Pseudomonas* species (sensu stricto) causing
'ginger blorch' disease of cultivated *Agaricus bisporus* using 16S
rRNA gene typing
JOURNAL
REFERENCE
2 (bases 1 to 1461)
Godfrey, S.A.C., Harrow, S.A., Marshall, J.W. and Klena, J.D.
Direct Submission
JOURNAL
Submitted (28-NOV-2000) Integrated Crop Protection, Crop & Food
Research Ltd., Private Bag 4704, Christchurch 8152, New Zealand
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RNA
/product="16S ribosomal RNA"
BASE COUNT 372 a 323 c 453 g 311 t 2 others

ORIGIN
Query Match 98.8%; Score 1057.2; DB 1; Length 1461;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1059; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 3 CCTGTCTCAGATGAAGCGTGGCGGCGCTTAACATGCAAGTGAAGCGGTAGAGAGA 62
Db 11 CTTGGCTCAGATGAAGCGTGGCGGCGCTTAACATGCAAGTGAAGCGGTAGAGAGA 70
Qy 63 AGCTTGCTTCTCTTGAAGCGCGGAGCGGTGAGTATGCTAGAAATCTGCTGTAGT 122
Db 71 AGCTTGCTTCTCTTGAAGCGCGGAGCGGTGAGTATGCTAGAAATCTGCTGTAGT 130
Qy 123 GGGGGAATACGTTGCGAAAGGACGCTAATACCGCATAGTCTCTAGCGGAAAGACAGG 182
Db 131 GGGGGAATACGTTGCGAAAGGACGCTAATACCGCATAGTCTCTAGCGGAAAGACAGG 190
Qy 183 GACCTTGCGGCTTGCCTATCAGATGAGCGCTAGTGCAGTTAGTGTGAGGATA 242
Db 191 GACCTTGCGGCTTGCCTATCAGATGAGCGCTAGTGCAGTTAGTGTGAGGATA 250

Qy 243 TGGCTCACCAAGGCGACGATCCGTAAGTGTCTGAGAGATGATCAGTCACTGTAAC 302
Db 251 TGGCTCACCAAGGCGACGATCCGTAAGTGTCTGAGAGATGATCAGTCACTGTAAC 310
Qy 303 GAGACACGCTCCAGACTCTTACGGAGCGACGATGGGAAATATTGGCAATGGCGAAA 362
Db 311 GAGACACGCTCCAGACTCTTACGGAGCGACGATGGGAAATATTGGCAATGGCGAAA 370
Qy 363 GCGTATCCAGACGATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 422
Db 371 GCGTATCCAGACGATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 430
Qy 423 TGGAGAAAGGCTTGAATTAATCTGCAATTTGACGTTACCGACAGATTAAGCAC 482
Db 431 TGGAGAAAGGCTTGAATTAATCTGCAATTTGACGTTACCGACAGATTAAGCAC 490
Qy 483 CGGCTAAGTCTGTGCGACGACCGCGGTATATCAGAGGCTCAGACGCTTATCGGA 542
Db 491 CGGCTAAGTCTGTGCGACGACCGCGGTATATCAGAGGCTCAGACGCTTATCGGA 550
Qy 543 CTGGGCGTAAAGCGCGCTAGGTGCTTTGTTAAGTGTGATGTAATCCCGGCTCAAC 602
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Qy 603 CTGGGAACTGCAATTAATACTGACTGACTAGATGTGTAAGGCTGTGAATTTCTG 662
Db 611 CTGGGAACTGCAATTAATACTGACTGACTAGATGTGTAAGGCTGTGAATTTCTG 670
Qy 663 TGTAGCGGTGAATGCGTATATGGAAGAAACACAGTGGCGAAGCGACACCTGGA 722
Db 671 TGTAGCGGTGAATGCGTATATGGAAGAAACACAGTGGCGAAGCGACACCTGGA 730
Qy 723 CTAAATCTGACACTGAGTGCAGAAACGTTGGGAGCAAAACAGATTAGATACCTGTAG 782
Db 731 CTAAATCTGACACTGAGTGCAGAAACGTTGGGAGCAAAACAGATTAGATACCTGTAG 790
Qy 783 TCCACCGCTTAAACGATGTCATGCTACCGCTTGAAGCCTTAGCTTTAGTGGGCGAG 842
Db 791 TCCACCGCTTAAACGATGTCATGCTACCGCTTGAAGCCTTAGCTTTAGTGGGCGAG 850
Qy 843 AACGCATTAGTGAACGCGCTGGGGAGTACGGCCGCAAGTTAAACTTAATGAATTGA 902
Db 851 AACGCATTAGTGAACGCGCTGGGGAGTACGGCCGCAAGTTAAACTTAATGAATTGA 910
Qy 903 CGGGGGCCCGCAACAAGCGGTGAGCAATGTGTTAATGAAACAACGGCAAGACTTTA 962
Db 911 CGGGGGCCCGCAACAAGCGGTGAGCAATGTGTTAATGAAACAACGGCAAGACTTTA 970
Qy 963 CCAGGCTTGAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1022
Db 971 CCAGGCTTGAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1030
Qy 1023 ACAGGTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1068
Db 1031 ACAGGTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1076

RESULT 9
LOCUS AF094729 1355 bp DNA linear BCT 04-OCT-2000
DEFINITION Pseudomonas fluorescens strain ATCC 17566 16S ribosomal RNA gene,
partial sequence.
ACCESSION AF094729
VERSION AF094729.1 GI:10567500
KEYWORDS
SOURCE Pseudomonas fluorescens
ORGANISM Pseudomonas fluorescens
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
REFERENCE
1 (bases 1 to 1355)
Galdier, M., Plasmeier, M.L., Blaine, L.D., Plante, P.A. and
Gilliver, P.M.
TITLE Comparison of Phenetic and Phylogenetic Classification Systems for